```
  951   TCCCTTAAGT  TT      AACTGGAA  AGATGTCGAG  CGGCTCGCTC
        AGGGAATTCA  AAC      CATTGACCTT  TCTACAGCTC  GCCGAGCGAG
-------------------------------------------------------------------------
 1001   ACAACCAGTC  GGTAGATGTC  AAGAAGAGAC  GTTGGGTTAC  CTTCTGCTCT
        TGTTGGTCAG  CCATCTACAG  TTCTTCTCTG  CAACCCAATG  GAAGACGAGA
-------------------------------------------------------------------------
 1051   GCAGAATGGC  CAACCTTTAA  CGTCGGATGG  CCGCGAGACG  GCACCTTTAA
        CGTCTTACCG  GTTGGAAATT  GCAGCCTACC  GGCGCTCTGC  CGTGGAAATT
-------------------------------------------------------------------------
 1101   CCGAGACCTC  ATCACCCAGG  TTAAGATCAA  GGTCTTTTCA  CCTGGCCCGC
        GGCTCTGGAG  TAGTGGGTCC  AATTCTAGTT  CCAGAAAAGT  GGACCGGGCG
-------------------------------------------------------------------------
 1151   ATGGACACCC  AGACCAGGTC  CCCTACATCG  TGACCTGGGA  AGCCTTGGCT
        TACCTGTGGG  TCTGGTCCAG  GGGATGTAGC  ACTGGACCCT  TCGGAACCGA
-------------------------------------------------------------------------
 1201   TTTGACCCCC  CTCCCTGGGT  CAAGCCCTTT  GTACACCCTA  AGCCTCCGCC
        AAACTGGGGG  GAGGGACCCA  GTTCGGGAAA  CATGTGGGAT  TCGGAGGCGG
-------------------------------------------------------------------------
 1251   TCCTCTTCCT  CCATCCGCCC  CGTCTCTCCC  CCTTGAACCT  CCTCGTTCGA
        AGGAGAAGGA  GGTAGGCGGG  GCAGAGAGGG  GGAACTTGGA  GGAGCAAGCT
-------------------------------------------------------------------------
 1301   CCCCGCCTCG  ATCCTCCCTT  TATCCAGCCC  TCACTCCTTC  TCTAGGCGCC
        GGGGCGGAGC  TAGGAGGGAA  ATAGGTCGGG  AGTGAGGAAG  AGATCCGCGG
-------------------------------------------------------------------------
 1351   GGCCGCTCTA  GCCCATTAAT  ACGACTCACT  ATAGGGCGAT  TCGAATCAGG
        CCGGCGAGAT  CGGGTAATTA  TGCTGAGTGA  TATCCCGCTA  AGCTTAGTCC
-------------------------------------------------------------------------
 1401   CCTTGGCGCG  CCGGATCCTT  AATTAAGCGC  AATTGGGAGG  TGGCGGTAGC
        GGAACCGCGC  GGCCTAGGAA  TTAATTCGCG  TTAACCCTCC  ACCGCCATCG
-------------------------------------------------------------------------
   +2            M   G   V   I   T   D   S   L   A   V   V   A   R   T   D
              ]-------------------------------------------------------
 1451   CTCGAGATGG  GCGTGATTAC  GGATTCACTG  GCCGTCGTGG  CCCGCACCGA
        GAGCTCTACC  CGCACTAATG  CCTAAGTGAC  CGGCAGCACC  GGGCGTGGCT
-------------------------------------------------------------------------
   +2   R   P   S   Q   Q   L   R   S   L   N   G   E   W   R   F   A
        -------------------------------------------------------------
 1501   TCGCCCTTCC  CAACAGTTAC  GCAGCCTGAA  TGGCGAATGG  CGCTTTGCCT
        AGCGGGAAGG  GTTGTCAATG  CGTCGGACTT  ACCGCTTACC  GCGAAACGGA
-------------------------------------------------------------------------
   +2 W   F   P   A   P   E   A   V   P   E   S   W   L   E   C   D   L
      -------------------------------------------------------------
 1551   GGTTTCCGGC  ACCAGAAGCG  GTGCCGGAAA  GCTGGCTGGA  GTGCGATCTT
        CCAAAGGCCG  TGGTCTTCGC  CACGGCCTTT  CGACCGACCT  CACGCTAGAA
-------------------------------------------------------------------------
   +2   P   E   A   D   T   V   V   V   P   S   N   W   Q   M   H   G   Y
        -------------------------------------------------------------
 1601   CCTGAGGCCG  ATACTGTCGT  CGTCCCCTCA  AACTGGCAGA  TGCACGGTTA
        GGACTCCGGC  TATGACAGCA  GCAGGGGAGT  TTGACCGTCT  ACGTGCCAAT
-------------------------------------------------------------------------
   +2   D   A   P   I   Y   T   N   V   T   Y   P   I   T   V   N   P
        -------------------------------------------------------------
 1651   CGATGCGCCC  ATCTACACCA  ACGTGACCTA  TCCCATTACG  GTCAATCCGC
        GCTACGCGGG  TAGATGTGGT  TGCACTGGAT  AGGGTAATGC  CAGTTAGGCG
```

FIG. 10C

```
    +2  P   F   V   P               P   T   G   C   Y   S   L   T   F   N
        -------------------------------------------------------------------
1701  CGTTTGTTCC CACGGAGAAT CCGACGGGTT GTTACTCGCT CACATTTAAT
      GCAAACAAGG GTGCCTCTTA GGCTGCCCAA CAATGAGCGA GTGTAAATTA
    -------------------------------------------------------------------------

    +2  V   D   E   S   W   L   Q   E   G   Q   T   R   I   I   F   D   G
        -------------------------------------------------------------------
1751  GTTGATGAAA GCTGGCTACA GGAAGGCCAG ACGCGAATTA TTTTTGATGG
      CAACTACTTT CGACCGATGT CCTTCCGGTC TGCGCTTAAT AAAAACTACC
    -------------------------------------------------------------------------

    +2  V   N   S   A   F   H   L   W   C   N   G   R   W   V   G   Y
        -------------------------------------------------------------------
1801  CGTTAACTCG GCGTTTCATC TGTGGTGCAA CGGGCGCTGG GTCGGTTACG
      GCAATTGAGC CGCAAAGTAG ACACCACGTT GCCCGCGACC CAGCCAATGC
    -------------------------------------------------------------------------

    +2 G   Q   D   S   R   L   P   S   E   F   D   L   S   A   F   L   R
        -------------------------------------------------------------------
1851  GCCAGGACAG TCGTTTGCCG TCTGAATTTG ACCTGAGCGC ATTTTTACGC
      CGGTCCTGTC AGCAAACGGC AGACTTAAAC TGGACTCGCG TAAAAATGCG
    -------------------------------------------------------------------------

    +2  A   G   E   N   R   L   A   V   M   V   L   R   W   S   D   G   S
        -------------------------------------------------------------------
1901  GCCGGAGAAA ACCGCCTCGC GGTGATGGTG CTGCGCTGGA GTGACGGCAG
      CGGCCTCTTT TGGCGGAGCG CCACTACCAC GACGCGACCT CACTGCCGTC
    -------------------------------------------------------------------------

    +2  Y   L   E   D   Q   D   M   W   R   M   S   G   I   F   R   D
        -------------------------------------------------------------------
1951  TTATCTGGAA GATCAGGATA TGTGGCGGAT GAGCGGCATT TTCCGTGACG
      AATAGACCTT CTAGTCCTAT ACACCGCCTA CTCGCCGTAA AAGGCACTGC
    -------------------------------------------------------------------------

    +2 V   S   L   L   H   K   P   T   T   Q   I   S   D   F   H   V   A
        -------------------------------------------------------------------
2001  TCTCGTTGCT GCATAAACCG ACTACACAAA TCAGCGATTT CCATGTTGCC
      AGAGCAACGA CGTATTTGGC TGATGTGTTT AGTCGCTAAA GGTACAACGG
    -------------------------------------------------------------------------

    +2  T   R   F   N   D   D   F   S   R   A   V   L   E   A   E   V   Q
        -------------------------------------------------------------------
2051  ACTCGCTTTA ATGATGATTT CAGCCGCGCT GTACTGGAGG CTGAAGTTCA
      TGAGCGAAAT TACTACTAAA GTCGGCGCGA CATGACCTCC GACTTCAAGT
    -------------------------------------------------------------------------

    +2  M   C   G   E   L   R   D   Y   L   R   V   T   V   S   L   W
        -------------------------------------------------------------------
2101  GATGTGCGGC GAGTTGCGTG ACTACCTACG GGTAACAGTT TCTTTATGGC
      CTACACGCCG CTCAACGCAC TGATGGATGC CCATTGTCAA AGAAATACCG
    -------------------------------------------------------------------------

    +2 Q   G   E   T   Q   V   A   S   G   T   A   P   F   G   G   E   I
        -------------------------------------------------------------------
2151  AGGGTGAAAC GCAGGTCGCC AGCGGCACCG CGCCTTTCGG CGGTGAAATT
      TCCCACTTTG CGTCCAGCGG TCGCCGTGGC GCGGAAAGCC GCCACTTTAA
    -------------------------------------------------------------------------

    +2  I   D   E   R   G   G   Y   A   D   R   V   T   L   R   L   N   V
        -------------------------------------------------------------------
2201  ATCGATGAGC GTGGTGGTTA TGCCGATCGC GTCACACTAC GTCTGAACGT
      TAGCTACTCG CACCACCAAT ACGGCTAGCG CAGTGTGATG CAGACTTGCA
    -------------------------------------------------------------------------

    +2  E   N   P   K   L   W   S   A   E   I   P   N   L   Y   R   A
        -------------------------------------------------------------------
2251  CGAAAACCCG AAACTGTGGA GCGCCGAAAT CCCGAATCTC TATCGTGCGG
      GCTTTTGGGC TTTGACACCT CGCGGCTTTA GGGCTTAGAG ATAGCACGCC
    -------------------------------------------------------------------------
```
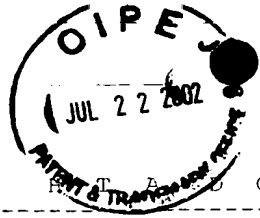
FIG. 10 D

```
   +2 V  V  E  L          T      G  T  L   I  E  A   E  A  C
      -------------------------------------------------------
2301  TGGTTGAACT GCACACCGCC GACGGCACGC TGATTGAAGC AGAAGCCTGC
      ACCAACTTGA CGTGTGGCGG CTGCCGTGCG ACTAACTTCG TCTTCGGACG
      -------------------------------------------------------

   +2  D  V  G  F  R  E  V   R  I  E   N  G  L  L   L  L  N
      -------------------------------------------------------
2351  GATGTCGGTT TCCGCGAGGT GCGGATTGAA AATGGTCTGC TGCTGCTGAA
      CTACAGCCAA AGGCGCTCCA CGCCTAACTT TTACCAGACG ACGACGACTT
      -------------------------------------------------------

   +2  G  K  P  L  L  I  R   G  V  N   R  H  E   H  H  P
      -------------------------------------------------------
2401  CGGCAAGCCG TTGCTGATTC GAGGCGTTAA CCGTCACGAG CATCATCCTC
      GCCGTTCGGC AACGACTAAG CTCCGCAATT GGCAGTGCTC GTAGTAGGAG
      -------------------------------------------------------

   +2  L  H  G  Q  V  M  D   E  Q  T  M  V  Q  D   I  L  L
      -------------------------------------------------------
2451  TGCATGGTCA GGTCATGGAT GAGCAGACGA TGGTGCAGGA TATCCTGCTG
      ACGTACCAGT CCAGTACCTA CTCGTCTGCT ACCACGTCCT ATAGGACGAC
      -------------------------------------------------------

   +2  M  K  Q  N  N  F  N   A  V  R   C  S  H  Y   P  N  H
      -------------------------------------------------------
2501  ATGAAGCAGA ACAACTTTAA CGCCGTGCGC TGTTCGCATT ATCCGAACCA
      TACTTCGTCT TGTTGAAATT GCGGCACGCG ACAAGCGTAA TAGGCTTGGT
      -------------------------------------------------------

   +2   P  L  W  Y  T  L  C   D  R  Y   G  L  Y   V  V  D
      -------------------------------------------------------
2551  TCCGCTGTGG TACACGCTGT GCGACCGCTA CGGCCTGTAT GTGGTGGATG
      AGGCGACACC ATGTGCGACA CGCTGGCGAT GCCGGACATA CACCACCTAC
      -------------------------------------------------------

   +2 E  A  N  I  E  T  H  G   M  V  P   M  N  R   L  T  D
      -------------------------------------------------------
2601  AAGCCAATAT TGAAACCCAC GGCATGGTGC CAATGAATCG TCTGACCGAT
      TTCGGTTATA ACTTTGGGTG CCGTACCACG GTTACTTAGC AGACTGGCTA
      -------------------------------------------------------

   +2  D  P  R  W  L  P  A   M  S  E   R  V  T  R   M  V  Q
      -------------------------------------------------------
2651  GATCCGCGCT GGCTACCGGC GATGAGCGAA CGCGTAACGC GAATGGTGCA
      CTAGGCGCGA CCGATGGCCG CTACTCGCTT GCGCATTGCG CTTACCACGT
      -------------------------------------------------------

   +2  R  D  R  N  H  P  S   V  I  I   W  S  L   G  N  E
      -------------------------------------------------------
2701  GCGCGATCGT AATCACCCGA GTGTGATCAT CTGGTCGCTG GGGAATGAAT
      CGCGCTAGCA TTAGTGGGCT CACACTAGTA GACCAGCGAC CCCTTACTTA
      -------------------------------------------------------

   +2 S  G  H  G  A  N  H  D   A  L  Y   R  W  I   K  S  V
      -------------------------------------------------------
2751  CAGGCCACGG CGCTAATCAC GACGCGCTGT ATCGCTGGAT CAAATCTGTC
      GTCCGGTGCC GCGATTAGTG CTGCGCGACA TAGCGACCTA GTTTAGACAG
      -------------------------------------------------------

   +2  D  P  S  R  P  V  Q   Y  E  G   G  G  A  D   T  T  A
      -------------------------------------------------------
2801  GATCCTTCCC GCCCGGTGCA GTATGAAGGC GGCGGAGCCG ACACCACGGC
      CTAGGAAGGG CGGGCCACGT CATACTTCCG CCGCCTCGGC TGTGGTGCCG
      -------------------------------------------------------

   +2  T  D  I  I  C  P  M   Y  A  R   V  D  E   D  Q  P
      -------------------------------------------------------
2851  CACCGATATT ATTTGCCCGA TGTACGCGCG CGTGGATGAA GACCAGCCCT
      GTGGCTATAA TAAACGGGCT ACATGCGCGC GCACCTACTT CTGGTCGGGA
      -------------------------------------------------------
```
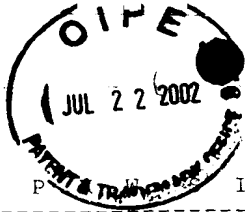
FIG. 10E

```
 +2 F  P  A  V   P  .  .  .   I  K  K   W  L  S   L  P  G
    ----------------------------------------------------------------
2901 TCCCGGCTGT GCCGAAATGG TCCATCAAAA AATGGCTTTC GCTACCTGGA
     AGGGCCGACA CGGCTTTACC AGGTAGTTTT TTACCGAAAG CGATGGACCT
    ----------------------------------------------------------------
 +2 E  T  R  P   L  I  L   C  E  Y   A  H  A  M   G  N  S
    ----------------------------------------------------------------
2951 GAGACGCGCC CGCTGATCCT TTGCGAATAC GCCCACGCGA TGGGTAACAG
     CTCTGCGCGG GCGACTAGGA AACGCTTATG CGGGTGCGCT ACCCATTGTC
    ----------------------------------------------------------------
 +2  L  G  G   F  A  K  Y   W  Q  A   F  R  Q   Y  P  R
    ----------------------------------------------------------------
3001 TCTTGGCGGT TTCGCTAAAT ACTGGCAGGC GTTTCGTCAG TATCCCCGTT
     AGAACCGCCA AAGCGATTTA TGACCGTCCG CAAAGCAGTC ATAGGGGCAA
    ----------------------------------------------------------------
 +2 L  Q  G  G   F  V  W   D  W  V  D   Q  S  L   I  K  Y
    ----------------------------------------------------------------
3051 TACAGGGCGG CTTCGTCTGG GACTGGGTGG ATCAGTCGCT GATTAAATAT
     ATGTCCCGCC GAAGCAGACC CTGACCCACC TAGTCAGCGA CTAATTTATA
    ----------------------------------------------------------------
 +2  D  E  N  G   N  P  W   S  A  Y   G  G  D  F   G  D  T
    ----------------------------------------------------------------
3101 GATGAAAACG GCAACCCGTG GTCGGCTTAC GGCGGTGATT TTGGCGATAC
     CTACTTTTGC CGTTGGGCAC CAGCCGAATG CCGCCACTAA AACCGCTATG
    ----------------------------------------------------------------
 +2  P  N  D  R   Q  F  C   M  N  G   L  V  F   A  D  R
    ----------------------------------------------------------------
3151 GCCGAACGAT CGCCAGTTCT GTATGAACGG TCTGGTCTTT GCCGACCGCA
     CGGCTTGCTA GCGGTCAAGA CATACTTGCC AGACCAGAAA CGGCTGGCGT
    ----------------------------------------------------------------
 +2 T  P  H  P   A  L  T   E  A  K  H   Q  Q  Q   F  F  Q
    ----------------------------------------------------------------
3201 CGCCGCATCC AGCGCTGACG GAAGCAAAAC ACCAGCAGCA GTTTTTCCAG
     GCGGCGTAGG TCGCGACTGC CTTCGTTTTG TGGTCGTCGT CAAAAAGGTC
    ----------------------------------------------------------------
 +2 F  R  L  S   G  Q  T   I  E  V   T  S  E  Y   L  F  R
    ----------------------------------------------------------------
3251 TTCCGTTTAT CCGGGCAAAC CATCGAAGTG ACCAGCGAAT ACCTGTTCCG
     AAGGCAAATA GGCCCGTTTG GTAGCTTCAC TGGTCGCTTA TGGACAAGGC
    ----------------------------------------------------------------
 +2  H  S  D   N  E  L  L   H  W  M   V  A  L   D  G  K
    ----------------------------------------------------------------
3301 TCATAGCGAT AACGAGCTCC TGCACTGGAT GGTGGCGCTG GATGGTAAGC
     AGTATCGCTA TTGCTCGAGG ACGTGACCTA CCACCGCGAC CTACCATTCG
    ----------------------------------------------------------------
 +2 P  L  A  S   G  E  V   P  L  D  V   A  P  Q   G  K  Q
    ----------------------------------------------------------------
3351 CGCTGGCAAG CGGTGAAGTG CCTCTGGATG TCGCTCCACA AGGTAAACAG
     GCGACCGTTC GCCACTTCAC GGAGACCTAC AGCGAGGTGT TCCATTTGTC
    ----------------------------------------------------------------
 +2 L  I  E  L   P  E  L   P  Q  P   E  S  A  G   Q  L  W
    ----------------------------------------------------------------
3401 TTGATTGAAC TGCCTGAACT ACCGCAGCCG GAGAGCGCCG GGCAACTCTG
     AACTAACTTG ACGGACTTGA TGGCGTCGGC CTCTCGCGGC CCGTTGAGAC
    ----------------------------------------------------------------
 +2 L  T  V  R   V  V  Q   P  N  A   T  A  W   S  E  A
    ----------------------------------------------------------------
3451 GCTCACAGTA CGCGTAGTGC AACCGAACGC GACCGCATGG TCAGAAGCCG
     CGAGTGTCAT GCGCATCACG TTGGCTTGCG CTGGCGTACC AGTCTTCGGC
    ----------------------------------------------------------------
```
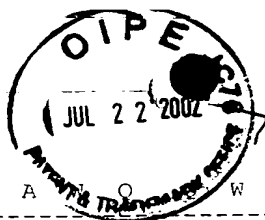
FIG. 1OF

FIGURE 10

```
   +2 G  H  I  S  A         Q    W  R  L  A  E  N  L  S  V
      ----------------------------------------------------
3501  GGCACATCAG CGCCTGGCAG CAGTGGCGTC TGGCGGAAAA CCTCAGTGTG
      CCGTGTAGTC GCGGACCGTC GTCACCGCAG ACCGCCTTTT GGAGTCACAC
```

```
   +2 T  L  P  A  A  S  H  A  I  P    H  L  T  T    S  E  M
      ----------------------------------------------------
3551  ACGCTCCCCG CCGCGTCCCA CGCCATCCCG CATCTGACCA CCAGCGAAAT
      TGCGAGGGGC GGCGCAGGGT GCGGTAGGGC GTAGACTGGT GGTCGCTTTA
```

```
   +2  D  F  C   I  E  L  G   N  K  R   W  Q  F   N  R  Q
      ----------------------------------------------------
3601  GGATTTTTGC ATCGAGCTGG GTAATAAGCG TTGGCAATTT AACCGCCAGT
      CCTAAAAACG TAGCTCGACC CATTATTCGC AACCGTTAAA TTGGCGGTCA
```

```
   +2 S  G  F  L   S  Q  M   W  I  G  D   K  K  Q   L  L  T
      ----------------------------------------------------
3651  CAGGCTTTCT TTCACAGATG TGGATTGGCG ATAAAAAACA ACTGCTGACG
      GTCCGAAAGA AAGTGTCTAC ACCTAACCGC TATTTTTTGT TGACGACTGC
```

```
   +2  P  L  R  D   Q  F  T   R  A  P   L  D  N  D   I  G  V
      ----------------------------------------------------
3701  CCGCTGCGCG ATCAGTTCAC CCGTGCACCG CTGGATAACG ACATTGGCGT
      GGCGACGCGC TAGTCAAGTG GGCACGTGGC GACCTATTGC TGTAACCGCA
```

```
   +2   S  E  A   T  R  I  D   P  N  A   W  V  E   R  W  K
      ----------------------------------------------------
3751  AAGTGAAGCG ACCCGCATTG ACCCTAACGC CTGGGTCGAA CGCTGGAAGG
      TTCACTTCGC TGGGCGTAAC TGGGATTGCG GACCCAGCTT GCGACCTTCC
```

```
   +2 A  A  G  H   Y  Q  A   E  A  A  L   L  Q  C   T  A  D
      ----------------------------------------------------
3801  CGGCGGGCCA TTACCAGGCC GAAGCAGCGT TGTTGCAGTG CACGGCAGAT
      GCCGCCCGGT AATGGTCCGG CTTCGTCGCA ACAACGTCAC GTGCCGTCTA
```

```
   +2 T  L  A  D   A  V  L   I  T  T   A  H  A  W   Q  H  Q
      ----------------------------------------------------
3851  ACACTTGCTG ATGCGGTGCT GATTACGACC GCTCACGCGT GGCAGCATCA
      TGTGAACGAC TACGCCACGA CTAATGCTGG CGAGTGCGCA CCGTCGTAGT
```

```
   +2  G  K  T   L  F  I  S   R  K  T   Y  R  I   D  G  S
      ----------------------------------------------------
3901  GGGGAAAACC TTATTTATCA GCCGGAAAAC CTACCGGATT GATGGTAGTG
      CCCCTTTTGG AATAAATAGT CGGCCTTTTG GATGGCCTAA CTACCATCAC
```

```
   +2 G  Q  M  A   I  T  V   D  V  E  V   A  S  D   T  P  H
      ----------------------------------------------------
3951  GTCAAATGGC GATTACCGTT GATGTTGAAG TGGCGAGCGA TACACCGCAT
      CAGTTTACCG CTAATGGCAA CTACAACTTC ACCGCTCGCT ATGTGGCGTA
```

```
   +2 P  A  R  I   G  L  N   C  Q  L   A  Q  V   A  E  R  V
      ----------------------------------------------------
4001  CCGGCGCGGA TTGGCCTGAA CTGCCAGCTG GCGCAGGTAG CAGAGCGGGT
      GGCCGCGCCT AACCGGACTT GACGGTCGAC CGCGTCCATC GTCTCGCCCA
```

```
   +2 N  W  L   G  L  G  P   Q  E  N   Y  P  D   R  L  T
      ----------------------------------------------------
4051  AAACTGGCTC GGATTAGGGC CGCAAGAAAA CTATCCCGAC CGCCTTACTG
      TTTGACCGAG CCTAATCCCG GCGTTCTTTT GATAGGGCTG GCGGAATGAC
```

FIG. 10G

```
     +2 A  A  C  F    D  R       D   L  P  L   S  D  M   Y  T  P
        ---------------------------------------------------------------
  4101 CCGCCTGTTT TGACCGCTGG GATCTGCCAT TGTCAGACAT GTATACCCCG
       GGCGGACAAA ACTGGCGACC CTAGACGGTA ACAGTCTGTA CATATGGGGC
        ---------------------------------------------------------------
     +2  Y  V  F  P  S  E  N    G  L  R   C  G  T  R   E  L  N
        ---------------------------------------------------------------
  4151 TACGTCTTCC CGAGCGAAAA CGGTCTGCGC TGCGGGACGC GCGAATTGAA
       ATGCAGAAGG GCTCGCTTTT GCCAGACGCG ACGCCCTGCG CGCTTAACTT
        ---------------------------------------------------------------
     +2   Y  G  P   H  Q  W  R  G  D  F   Q  F  N   I  S  R
        ---------------------------------------------------------------
  4201 TTATGGCCCA CACCAGTGGC GCGGCGACTT CCAGTTCAAC ATCAGCCGCT
       AATACCGGGT GTGGTCACCG CGCCGCTGAA GGTCAAGTTG TAGTCGGCGA
        ---------------------------------------------------------------
     +2 Y  S  Q  Q   Q  L  M   E  T  S   H  R  H  L   L  H  A
        ---------------------------------------------------------------
  4251 ACAGTCAACA GCAACTGATG GAAACCAGCC ATCGCCATCT GCTGCACGCG
       TGTCAGTTGT CGTTGACTAC CTTTGGTCGG TAGCGGTAGA CGACGTGCGC
        ---------------------------------------------------------------
     +2  E  E  G  T   W  L  N   I  D  G   F  H  M  G   I  G  G
        ---------------------------------------------------------------
  4301 GAAGAAGGCA CATGGCTGAA TATCGACGGT TTCCATATGG GGATTGGTGG
       CTTCTTCCGT GTACCGACTT ATAGCTGCCA AAGGTATACC CCTAACCACC
        ---------------------------------------------------------------
     +2   D  D  S   W  S  P  S  V  S  A   E  F  Q   L  S  A
        ---------------------------------------------------------------
  4351 CGACGACTCC TGGAGCCCGT CAGTATCGGC GGAATTCCAG CTGAGCGCCG
       GCTGCTGAGG ACCTCGGGCA GTCATAGCCG CCTTAAGGTC GACTCGCGGC
        ---------------------------------------------------------------
     +2 G  R  Y  H   Y  Q  L   V  W  C  Q   K  R  S   D  Y  K
        ---------------------------------------------------------------
  4401 GTCGCTACCA TTACCAGTTG GTCTGGTGTC AAAAAAGATC TGACTATAAA
       CAGCGATGGT AATGGTCAAC CAGACCACAG TTTTTTCTAG ACTGATATTT
        ---------------------------------------------------------------
     +2   D  E  D  L   D  H  H    H  H  H    H  R
        -------------------------------------------------->
  4451 GATGAGGACC TCGACCATCA TCATCATCAT CACCGGTAAT AATAGGTAGA
       CTACTCCTGG AGCTGGTAGT AGTAGTAGTA GTGGCCATTA TTATCCATCT
        ---------------------------------------------------------------
  4501 TAAGTGACTG ATTAGATGCA TTGATCCCTC GACCAATTCC GGTTATTTTC
       ATTCACTGAC TAATCTACGT AACTAGGGAG CTGGTTAAGG CCAATAAAAG
        ---------------------------------------------------------------
  4551 CACCATATTG CCGTCTTTTG GCAATGTGAG GGCCCGGAAA CCTGGCCCTG
       GTGGTATAAC GGCAGAAAAC CGTTACACTC CCGGGCCTTT GGACCGGGAC
        ---------------------------------------------------------------
  4601 TCTTCTTGAC GAGCATTCCT AGGGGTCTTT CCCCTCTCGC CAAAGGAATG
       AGAAGAACTG CTCGTAAGGA TCCCCAGAAA GGGGAGAGCG GTTTCCTTAC
        ---------------------------------------------------------------
  4651 CAAGGTCTGT TGAATGTCGT GAAGGAAGCA GTTCCTCTGG AAGCTTCTTG
       GTTCCAGACA ACTTACAGCA CTTCCTTCGT CAAGGAGACC TTCGAAGAAC
        ---------------------------------------------------------------
  4701 AAGACAAACA ACGTCTGTAG CGACCCTTTG CAGGCAGCGG AACCCCCCAC
       TTCTGTTTGT TGCAGACATC GCTGGGAAAC GTCCGTCGCC TTGGGGGGTG
        ---------------------------------------------------------------
  4751 CTGGCGACAG GTGCCTCTGC GGCCAAAAGC CACGTGTATA AGATACACCT
       GACCGCTGTC CACGGAGACG CCGGTTTTCG GTGCACATAT TCTATGTGGA
        ---------------------------------------------------------------
```

FIG. 10H

```
5751   GGCTGACCGC  TTCCTCGTGC  ........AT  CGCCGCTCCC  GATTCGCAGC
       CCGACTGGCG  AAGGAGCACG  AAATGCCATA  GCGGCGAGGG  CTAAGCGTCG
```
- -
```
5801   GCATCGCCTT  CTATCGCCTT  CTTGACGAGT  TCTTCTGAGC  GGGACTCTGG
       CGTAGCGGAA  GATAGCGGAA  GAACTGCTCA  AGAAGACTCG  CCCTGAGACC
```
- -
```
5851   GGTTCGCATC  GATAAAATAA  AAGATTTTAT  TTAGTCTCCA  GAAAAAGGGG
       CCAAGCGTAG  CTATTTTATT  TTCTAAAATA  AATCAGAGGT  CTTTTTCCCC
```
- -
```
5901   GGAATGAAAG  ACCCCACCTG  TAGGTTTGGC  AAGCTAGCTT  AAGTAACGCC
       CCTTACTTTC  TGGGGTGGAC  ATCCAAACCG  TTCGATCGAA  TTCATTGCGG
```
- -
```
5951   ATTTTGCAAG  GCATGGAAAA  ATACATAACT  GAGAATAGAG  AAGTTCAGAT
       TAAAACGTTC  CGTACCTTTT  TATGTATTGA  CTCTTATCTC  TTCAAGTCTA
```
- -
```
6001   CAAGGTCAGG  AACAGATGGA  ACAGCTGAAT  ATGGGCCAAA  CAGGATATCT
       GTTCCAGTCC  TTGTCTACCT  TGTCGACTTA  TACCCGGTTT  GTCCTATAGA
```
- -
```
6051   GTGGTAAGCA  GTTCCTGCCC  CGGCTCAGGG  CCAAGAACAG  ATGGAACAGC
       CACCATTCGT  CAAGGACGGG  GCCGAGTCCC  GGTTCTTGTC  TACCTTGTCG
```
- -
```
6101   TGAATATGGG  CCAAACAGGA  TATCTGTGGT  AAGCAGTTCC  TGCCCCGGCT
       ACTTATACCC  GGTTTGTCCT  ATAGACACCA  TTCGTCAAGG  ACGGGGCCGA
```
- -
```
6151   CAGGGCCAAG  AACAGATGGT  CCCCAGATGC  GGTCCAGCCC  TCAGCAGTTT
       GTCCCGGTTC  TTGTCTACCA  GGGGTCTACG  CCAGGTCGGG  AGTCGTCAAA
```
- -
```
6201   CTAGAGAACC  ATCAGATGTT  TCCAGGGTGC  CCCAAGGACC  TGAAATGACC
       GATCTCTTGG  TAGTCTACAA  AGGTCCCACG  GGGTTCCTGG  ACTTTACTGG
```
- -
```
6251   CTGTGCCTTA  TTTGAACTAA  CCAATCAGTT  CGCTTCTCGC  TTCTGTTCGC
       GACACGGAAT  AAACTTGATT  GGTTAGTCAA  GCGAAGAGCG  AAGACAAGCG
```
- -
```
6301   GCGCTTCTGC  TCCCCGAGCT  CAATAAAAGA  GCCCACAACC  CCTCACTCGG
       CGCGAAGACG  AGGGGCTCGA  GTTATTTTCT  CGGGTGTTGG  GGAGTGAGCC
```
- -
```
6351   GGCGCCAGTC  CTCCGATTGA  CTGAGTCGCC  CGGGTACCCG  TGTATCCAAT
       CCGCGGTCAG  GAGGCTAACT  GACTCAGCGG  GCCCATGGGC  ACATAGGTTA
```
- -
```
6401   AAACCCTCTT  GCAGTTGCAT  CCGACTTGTG  GTCTCGCTGT  TCCTTGGGAG
       TTTGGGAGAA  CGTCAACGTA  GGCTGAACAC  CAGAGCGACA  AGGAACCCTC
```
- -
```
6451   GGTCTCCTCT  GAGTGATTGA  CTACCCGTCA  GCGGGGGTCT  TTCATTCATG
       CCAGAGGAGA  CTCACTAACT  GATGGGCAGT  CGCCCCCAGA  AAGTAAGTAC
```
- -
```
6501   CAGCATGTAT  CAAAATTAAT  TTGGTTTTTT  TTCTTAAGTA  TTTACATTAA
       GTCGTACATA  GTTTTAATTA  AACCAAAAAA  AAGAATTCAT  AAATGTAATT
```
- -
```
6551   ATGGCCATAG  TTGCATTAAT  GAATCGGCCA  ACGCGCGGGG  AGAGGCGGTT
       TACCGGTATC  AACGTAATTA  CTTAGCCGGT  TGCGCGCCCC  TCTCCGCCAA
```
- -
```
6601   TGCGTATTGG  CGCTCTTCCG  CTTCCTCGCT  CACTGACTCG  CTGCGCTCGG
       ACGCATAACC  GCGAGAAGGC  GAAGGAGCGA  GTGACTGAGC  GACGCGAGCC
```
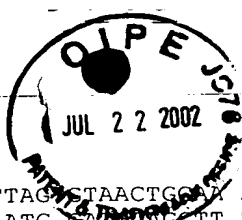- -
```
6651   TCGTTCGGCT  GCGGCGAGCG  GTATCAGCTC  ACTCAAAGGC  GGTAATACGG
       AGCAAGCCGA  CGCCGCTCGC  CATAGTCGAG  TGAGTTTCCG  CCATTATGCC
```
- -

FIG. 10 I

```
 951   TCCCTTAAGT TTGACCTTAG  TAACTGG    AGATGTCGAG CGGCTCGCTC
       AGGGAATTCA AACTGGAATC           TT TCTACAGCTC GCCGAGCGAG
------------------------------------------------------------

1001   ACAACCAGTC GGTAGATGTC AAGAAGAGAC GTTGGGTTAC CTTCTGCTCT
       TGTTGGTCAG CCATCTACAG TTCTTCTCTG CAACCCAATG GAAGACGAGA
------------------------------------------------------------

1051   GCAGAATGGC CAACCTTTAA CGTCGGATGG CCGCGAGACG GCACCTTTAA
       CGTCTTACCG GTTGGAAATT GCAGCCTACC GGCGCTCTGC CGTGGAAATT
------------------------------------------------------------

1101   CCGAGACCTC ATCACCCAGG TTAAGATCAA GGTCTTTTCA CCTGGCCCGC
       GGCTCTGGAG TAGTGGGTCC AATTCTAGTT CCAGAAAAGT GGACCGGGCG
------------------------------------------------------------

1151   ATGGACACCC AGACCAGGTC CCCTACATCG TGACCTGGGA AGCCTTGGCT
       TACCTGTGGG TCTGGTCCAG GGGATGTAGC ACTGGACCCT TCGGAACCGA
------------------------------------------------------------

1201   TTTGACCCCC CTCCCTGGGT CAAGCCCTTT GTACACCCTA AGCCTCCGCC
       AAACTGGGGG GAGGGACCCA GTTCGGGAAA CATGTGGGAT TCGGAGGCGG
------------------------------------------------------------

1251   TCCTCTTCCT CCATCCGCCC CGTCTCTCCC CCTTGAACCT CCTCGTTCGA
       AGGAGAAGGA GGTAGGCGGG GCAGAGAGGG GGAACTTGGA GGAGCAAGCT
------------------------------------------------------------

1301   CCCCGCCTCG ATCCTCCCTT TATCCAGCCC TCACTCCTTC TCTAGGCGCC
       GGGGCGGAGC TAGGAGGGAA ATAGGTCGGG AGTGAGGAAG AGATCCGCGG
------------------------------------------------------------

1351   GGCCGCTCTA GCCCATTAAT ACGACTCACT ATAGGGCGAT TCGAACACCA
       CCGGCGAGAT CGGGTAATTA TGCTGAGTGA TATCCCGCTA AGCTTGTGGT
------------------------------------------------------------

1401   TGCACCATCA TCATCATCAC GTCGACTATA AAGATGAGGA CCTCGAGATG
       ACGTGGTAGT AGTAGTAGTG CAGCTGATAT TTCTACTCCT GGAGCTCTAC
------------------------------------------------------------

1451   GGCGTGATTA CGGATTCACT GGCCGTCGTG GCCCGCACCG ATCGCCCTTC
       CCGCACTAAT GCCTAAGTGA CCGGCAGCAC CGGGCGTGGC TAGCGGGAAG
------------------------------------------------------------

1501   CCAACAGTTA CGCAGCCTGA ATGGCGAATG GCGCTTTGCC TGGTTTCCGG
       GGTTGTCAAT GCGTCGGACT TACCGCTTAC CGCGAAACGG ACCAAAGGCC
------------------------------------------------------------

1551   CACCAGAAGC GGTGCCGGAA AGCTGGCTGG AGTGCGATCT TCCTGAGGCC
       GTGGTCTTCG CCACGGCCTT TCGACCGACC TCACGCTAGA AGGACTCCGG
------------------------------------------------------------

1601   GATACTGTCG TCGTCCCCTC AAACTGGCAG ATGCACGGTT ACGATGCGCC
       CTATGACAGC AGCAGGGGAG TTTGACCGTC TACGTGCCAA TGCTACGCGG
------------------------------------------------------------

1651   CATCTACACC AACGTGACCT ATCCCATTAC GGTCAATCCG CCGTTTGTTC
       GTAGATGTGG TTGCACTGGA TAGGGTAATG CCAGTTAGGC GGCAAACAAG
------------------------------------------------------------

1701   CCACGGAGAA TCCGACGGGT TGTTACTCGC TCACATTTAA TGTTGATGAA
       GGTGCCTCTT AGGCTGCCCA ACAATGAGCG AGTGTAAATT ACAACTACTT
------------------------------------------------------------

1751   AGCTGGCTAC AGGAAGGCCA GACGCGAATT ATTTTTGATG GCGTTAACTC
       TCGACCGATG TCCTTCCGGT CTGCGCTTAA TAAAAACTAC CGCAATTGAG
------------------------------------------------------------

1801   GGCGTTTCAT CTGTGGTGCA ACGGGCGCTG GGTCGGTTAC GGCCAGGACA
       CCGCAAAGTA GACACCACGT TGCCCGCGAC CCAGCCAATG CCGGTCCTGT
------------------------------------------------------------

1851   GTCGTTTGCC GTCTGAATTT GACCTGAGCG CATTTTTACG CGCCGGAGAA
       CAGCAAACGG CAGACTTAAA CTGGACTCGC GTAAAAATGC GCGGCCTCTT
------------------------------------------------------------
```

FIG. IIC

```
1901   AACCGCCTCG  CGGTGATGGT  GCTTGGCTGG  AGTGACGGCA  GTTATCTGGA
       TTGGCGGAGC  GCCACTACCA  CGACGCGACC  TCACTGCCGT  CAATAGACCT
------------------------------------------------------------------
1951   AGATCAGGAT  ATGTGGCGGA  TGAGCGGCAT  TTTCCGTGAC  GTCTCGTTGC
       TCTAGTCCTA  TACACCGCCT  ACTCGCCGTA  AAAGGCACTG  CAGAGCAACG
------------------------------------------------------------------
2001   TGCATAAACC  GACTACACAA  ATCAGCGATT  TCCATGTTGC  CACTCGCTTT
       ACGTATTTGG  CTGATGTGTT  TAGTCGCTAA  AGGTACAACG  GTGAGCGAAA
------------------------------------------------------------------
2051   AATGATGATT  TCAGCCGCGC  TGTACTGGAG  GCTGAAGTTC  AGATGTGCGG
       TTACTACTAA  AGTCGGCGCG  ACATGACCTC  CGACTTCAAG  TCTACACGCC
------------------------------------------------------------------
2101   CGAGTTGCGT  GACTACCTAC  GGGTAACAGT  TTCTTTATGG  CAGGGTGAAA
       GCTCAACGCA  CTGATGGATG  CCCATTGTCA  AAGAAATACC  GTCCCACTTT
------------------------------------------------------------------
2151   CGCAGGTCGC  CAGCGGCACC  GCGCCTTTCG  GCGGTGAAAT  TATCGATGAG
       GCGTCCAGCG  GTCGCCGTGG  CGCGGAAAGC  CGCCACTTTA  ATAGCTACTC
------------------------------------------------------------------
2201   CGTGGTGGTT  ATGCCGATCG  CGTCACACTA  CGTCTGAACG  TCGAAAACCC
       GCACCACCAA  TACGGCTAGC  GCAGTGTGAT  GCAGACTTGC  AGCTTTTGGG
------------------------------------------------------------------
2251   GAAACTGTGG  AGCGCCGAAA  TCCCGAATCT  CTATCGTGCG  GTGGTTGAAC
       CTTTGACACC  TCGCGGCTTT  AGGGCTTAGA  GATAGCACGC  CACCAACTTG
------------------------------------------------------------------
2301   TGCACACCGC  CGACGGCACG  CTGATTGAAG  CAGAAGCCTG  CGATGTCGGT
       ACGTGTGGCG  GCTGCCGTGC  GACTAACTTC  GTCTTCGGAC  GCTACAGCCA
------------------------------------------------------------------
2351   TTCCGCGAGG  TGCGGATTGA  AAATGGTCTG  CTGCTGCTGA  ACGGCAAGCC
       AAGGCGCTCC  ACGCCTAACT  TTTACCAGAC  GACGACGACT  TGCCGTTCGG
------------------------------------------------------------------
2401   GTTGCTGATT  CGAGGCGTTA  ACCGTCACGA  GCATCATCCT  CTGCATGGTC
       CAACGACTAA  GCTCCGCAAT  TGGCAGTGCT  CGTAGTAGGA  GACGTACCAG
------------------------------------------------------------------
2451   AGGTCATGGA  TGAGCAGACG  ATGGTGCAGG  ATATCCTGCT  GATGAAGCAG
       TCCAGTACCT  ACTCGTCTGC  TACCACGTCC  TATAGGACGA  CTACTTCGTC
------------------------------------------------------------------
2501   AACAACTTTA  ACGCCGTGCG  CTGTTCGCAT  TATCCGAACC  ATCCGCTGTG
       TTGTTGAAAT  TGCGGCACGC  GACAAGCGTA  ATAGGCTTGG  TAGGCGACAC
------------------------------------------------------------------
2551   GTACACGCTG  TGCGACCGCT  ACGGCCTGTA  TGTGGTGGAT  GAAGCCAATA
       CATGTGCGAC  ACGCTGGCGA  TGCCGGACAT  ACACCACCTA  CTTCGGTTAT
------------------------------------------------------------------
2601   TTGAAACCCA  CGGCATGGTG  CCAATGAATC  GTCTGACCGA  TGATCCGCGC
       AACTTTGGGT  GCCGTACCAC  GGTTACTTAG  CAGACTGGCT  ACTAGGCGCG
------------------------------------------------------------------
2651   TGGCTACCGG  CGATGAGCGA  ACGCGTAACG  CGAATGGTGC  AGCGCGATCG
       ACCGATGGCC  GCTACTCGCT  TGCGCATTGC  GCTTACCACG  TCGCGCTAGC
------------------------------------------------------------------
2701   TAATCACCCG  AGTGTGATCA  TCTGGTCGCT  GGGGAATGAA  TCAGGCCACG
       ATTAGTGGGC  TCACACTAGT  AGACCAGCGA  CCCCTTACTT  AGTCCGGTGC
------------------------------------------------------------------
2751   GCGCTAATCA  CGACGCGCTG  TATCGCTGGA  TCAAATCTGT  CGATCCTTCC
       CGCGATTAGT  GCTGCGCGAC  ATAGCGACCT  AGTTTAGACA  GCTAGGAAGG
------------------------------------------------------------------
2801   CGCCCGGTGC  AGTATGAAGG  CGGCGGAGCC  GACACCACGG  CCACCGATAT
       GCGGGCCACG  TCATACTTCC  GCCGCCTCGG  CTGTGGTGCC  GGTGGCTATA
------------------------------------------------------------------
```

FIG. 11D

```
2851   TATTTGCCCG ATGTACGCGC ...GA AGACCAGCCC TTCCCGGCTG
       ATAAACGGGC TACATGCGCG CGCACCTACT TCTGGTCGGG AAGGGCCGAC

-------------------------------------------------------------

2901   TGCCGAAATG GTCCATCAAA AAATGGCTTT CGCTACCTGG AGAGACGCGC
       ACGGCTTTAC CAGGTAGTTT TTTACCGAAA GCGATGGACC TCTCTGCGCG

-------------------------------------------------------------

2951   CCGCTGATCC TTTGCGAATA CGCCCACGCG ATGGGTAACA GTCTTGGCGG
       GGCGACTAGG AAACGCTTAT GCGGGTGCGC TACCCATTGT CAGAACCGCC

-------------------------------------------------------------

3001   TTTCGCTAAA TACTGGCAGG CGTTTCGTCA GTATCCCCGT TTACAGGGCG
       AAAGCGATTT ATGACCGTCC GCAAAGCAGT CATAGGGGCA AATGTCCCGC

-------------------------------------------------------------

3051   GCTTCGTCTG GGACTGGGTG GATCAGTCGC TGATTAAATA TGATGAAAAC
       CGAAGCAGAC CCTGACCCAC CTAGTCAGCG ACTAATTTAT ACTACTTTTG

-------------------------------------------------------------

3101   GGCAACCCGT GGTCGGCTTA CGGCGGTGAT TTTGGCGATA CGCCGAACGA
       CCGTTGGGCA CCAGCCGAAT GCCGCCACTA AAACCGCTAT GCGGCTTGCT

-------------------------------------------------------------

3151   TCGCCAGTTC TGTATGAACG GTCTGGTCTT TGCCGACCGC ACGCCGCATC
       AGCGGTCAAG ACATACTTGC CAGACCAGAA ACGGCTGGCG TGCGGCGTAG

-------------------------------------------------------------

3201   CAGCGCTGAC GGAAGCAAAA CACCAGCAGC AGTTTTTCCA GTTCCGTTTA
       GTCGCGACTG CCTTCGTTTT GTGGTCGTCG TCAAAAAGGT CAAGGCAAAT

-------------------------------------------------------------

3251   TCCGGGCAAA CCATCGAAGT GACCAGCGAA TACCTGTTCC GTCATAGCGA
       AGGCCCGTTT GGTAGCTTCA CTGGTCGCTT ATGGACAAGG CAGTATCGCT

-------------------------------------------------------------

3301   TAACGAGCTC CTGCACTGGA TGGTGGCGCT GGATGGTAAG CCGCTGGCAA
       ATTGCTCGAG GACGTGACCT ACCACCGCGA CCTACCATTC GGCGACCGTT

-------------------------------------------------------------

3351   GCGGTGAAGT GCCTCTGGAT GTCGCTCCAC AAGGTAAACA GTTGATTGAA
       CGCCACTTCA CGGAGACCTA CAGCGAGGTG TTCCATTTGT CAACTAACTT

-------------------------------------------------------------

3401   CTGCCTGAAC TACCGCAGCC GGAGAGCGCC GGGCAACTCT GGCTCACAGT
       GACGGACTTG ATGGCGTCGG CCTCTCGCGG CCCGTTGAGA CCGAGTGTCA

-------------------------------------------------------------

3451   ACGCGTAGTG CAACCGAACG CGACCGCATG GTCAGAAGCC GGGCACATCA
       TGCGCATCAC GTTGGCTTGC GCTGGCGTAC CAGTCTTCGG CCCGTGTAGT

-------------------------------------------------------------

3501   GCGCCTGGCA GCAGTGGCGT CTGGCGGAAA ACCTCAGTGT GACGCTCCCC
       CGCGGACCGT CGTCACCGCA GACCGCCTTT TGGAGTCACA CTGCGAGGGG

-------------------------------------------------------------

3551   GCCGCGTCCC ACGCCATCCC GCATCTGACC ACCAGCGAAA TGGATTTTTG
       CGGCGCAGGG TGCGGTAGGG CGTAGACTGG TGGTCGCTTT ACCTAAAAAC

-------------------------------------------------------------

3601   CATCGAGCTG GGTAATAAGC GTTGGCAATT TAACCGCCAG TCAGGCTTTC
       GTAGCTCGAC CCATTATTCG CAACCGTTAA ATTGGCGGTC AGTCCGAAAG

-------------------------------------------------------------

3651   TTTCACAGAT GTGGATTGGC GATAAAAAAC AACTGCTGAC GCCGCTGCGC
       AAAGTGTCTA CACCTAACCG CTATTTTTTG TTGACGACTG CGGCGACGCG

-------------------------------------------------------------

3701   GATCAGTTCA CCCGTGCACC GCTGGATAAC GACATTGGCG TAAGTGAAGC
       CTAGTCAAGT GGGCACGTGG CGACCTATTG CTGTAACCGC ATTCACTTCG

-------------------------------------------------------------

3751   GACCCGCATT GACCCTAACG CCTGGGTCGA ACGCTGGAAG GCGGCGGGCC
       CTGGGCGTAA CTGGGATTGC GGACCCAGCT TGCGACCTTC CGCCGCCCGG

-------------------------------------------------------------
```

FIG. 11E

```
3801  ATTACCAGGC CGAAGCAG.. ..TG....CAGT GCACGGCAGA TACACTTGCT
      TAATGGTCCG GCTTCGTCGC ..CAACGTCA CGTGCCGTCT ATGTGAACGA
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
3851  GATGCGGTGC TGATTACGAC CGCTCACGCG TGGCAGCATC AGGGGAAAAC
      CTACGCCACG ACTAATGCTG GCGAGTGCGC ACCGTCGTAG TCCCCTTTTG
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
3901  CTTATTTATC AGCCGGAAAA CCTACCGGAT TGATGGTAGT GGTCAAATGG
      GAATAAATAG TCGGCCTTTT GGATGGCCTA ACTACCATCA CCAGTTTACC
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
3951  CGATTACCGT TGATGTTGAA GTGGCGAGCG ATACACCGCA TCCGGCGCGG
      GCTAATGGCA ACTACAACTT CACCGCTCGC TATGTGGCGT AGGCCGCGCC
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
4001  ATTGGCCTGA ACTGCCAGCT GGCGCAGGTA GCAGAGCGGG TAAACTGGCT
      TAACCGGACT TGACGGTCGA CCGCGTCCAT CGTCTCGCCC ATTTGACCGA
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
4051  CGGATTAGGG CCGCAAGAAA ACTATCCCGA CCGCCTTACT GCCGCCTGTT
      GCCTAATCCC GGCGTTCTTT TGATAGGGCT GGCGGAATGA CGGCGGACAA
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
4101  TTGACCGCTG GGATCTGCCA TTGTCAGACA TGTATACCCC GTACGTCTTC
      AACTGGCGAC CCTAGACGGT AACAGTCTGT ACATATGGGG CATGCAGAAG
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
4151  CCGAGCGAAA ACGGTCTGCG CTGCGGGACG CGCGAATTGA ATTATGGCCC
      GGCTCGCTTT TGCCAGACGC GACGCCCTGC GCGCTTAACT TAATACCGGG
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
4201  ACACCAGTGG CGCGGCGACT TCCAGTTCAA CATCAGCCGC TACAGTCAAC
      TGTGGTCACC GCGCCGCTGA AGGTCAAGTT GTAGTCGGCG ATGTCAGTTG
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
4251  AGCAACTGAT GGAAACCAGC CATCGCCATC TGCTGCACGC GGAAGAAGGC
      TCGTTGACTA CCTTTGGTCG GTAGCGGTAG ACGACGTGCG CCTTCTTCCG
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
4301  ACATGGCTGA ATATCGACGG TTTCCATATG GGGATTGGTG GCGACGACTC
      TGTACCGACT TATAGCTGCC AAAGGTATAC CCCTAACCAC CGCTGCTGAG
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
4351  CTGGAGCCCG TCAGTATCGG CGGAATTCCA GCTGAGCGCC GGTCGCTACC
      GACCTCGGGC AGTCATAGCC GCCTTAAGGT CGACTCGCGG CCAGCGATGG
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
4401  ATTACCAGTT GGTCTGGTGT CAAAAAAGAT CTGGAGGTGG TGGCAGCAGG
      TAATGGTCAA CCAGACCACA GTTTTTTCTA GACCTCCACC ACCGTCGTCC
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
4451  CCTTGGCGCG CCGGATCCTT AATTAACAAT TGACCGGTAA TAATAGGTAG
      GGAACCGCGC GGCCTAGGAA TTAATTGTTA ACTGGCCATT ATTATCCATC
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
4501  ATAAGTGACT GATTAGATGC ATTGATCCCT CGACCAATTC CGGTTATTTT
      TATTCACTGA CTAATCTACG TAACTAGGGA GCTGGTTAAG GCCAATAAAA
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
4551  CCACCATATT GCCGTCTTTT GGCAATGTGA GGGCCCGGAA ACCTGGCCCT
      GGTGGTATAA CGGCAGAAAA CCGTTACACT CCCGGGCCTT TGGACCGGGA
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
4601  GTCTTCTTGA CGAGCATTCC TAGGGGTCTT TCCCCTCTCG CCAAAGGAAT
      CAGAAGAACT GCTCGTAAGG ATCCCCAGAA AGGGGAGAGC GGTTTCCTTA
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
4651  GCAAGGTCTG TTGAATGTCG TGAAGGAAGC AGTTCCTCTG GAAGCTTCTT
      CGTTCCAGAC AACTTACAGC ACTTCCTTCG TCAAGGAGAC CTTCGAAGAA
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
4701  GAAGACAAAC AACGTCTGTA GCGACCCTTT GCAGGCAGCG GAACCCCCCA
      CTTCTGTTTG TTGCAGACAT CGCTGGGAAA CGTCCGTCGC CTTGGGGGGT
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
```
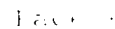
FIG. 11F

```
4751   CCTGGCGACA  GGTGCCTCTG  GCCCAGCAG  CCACGTGTAT  AAGATACACC
       GGACCGCTGT  CCACGGAGAC  GCCGGTTTTC  GGTGCACATA  TTCTATGTGG
-------------------------------------------------------------------

4801   TGCAAAGGCG  GCACAACCCC  AGTGCCACGT  TGTGAGTTGG  ATAGTTGTGG
       ACGTTTCCGC  CGTGTTGGGG  TCACGGTGCA  ACACTCAACC  TATCAACACC
-------------------------------------------------------------------

4851   AAAGAGTCAA  ATGGCTCTCC  TCAAGCGTAT  TCAACAAGGG  GCTGAAGGAT
       TTTCTCAGTT  TACCGAGAGG  AGTTCGCATA  AGTTGTTCCC  CGACTTCCTA
-------------------------------------------------------------------

4901   GCCCAGAAGG  TACCCCATTG  TATGGGATCT  GATCTGGGGC  CTCGGTGCAC
       CGGGTCTTCC  ATGGGGTAAC  ATACCCTAGA  CTAGACCCCG  GAGCCACGTG
-------------------------------------------------------------------

4951   ATGCTTTACA  TGTGTTTAGT  CGAGGTTAAA  AAACGTCTAG  GCCCCCCGAA
       TACGAAATGT  ACACAAATCA  GCTCCAATTT  TTTGCAGATC  CGGGGGGCTT
-------------------------------------------------------------------

5001   CCACGGGGAC  GTGGTTTTCC  TTTGAAAAAC  ACGATGATAA  TACCATGATT
       GGTGCCCCTG  CACCAAAAGG  AAACTTTTTG  TGCTACTATT  ATGGTACTAA
-------------------------------------------------------------------

5051   GAACAAGATG  GATTGCACGC  AGGTTCTCCG  GCCGCTTGGG  TGGAGAGGCT
       CTTGTTCTAC  CTAACGTGCG  TCCAAGAGGC  CGGCGAACCC  ACCTCTCCGA
-------------------------------------------------------------------

5101   ATTCGGCTAT  GACTGGGCAC  AACAGACAAT  CGGCTGCTCT  GATGCCGCCG
       TAAGCCGATA  CTGACCCGTG  TTGTCTGTTA  GCCGACGAGA  CTACGGCGGC
-------------------------------------------------------------------

5151   TGTTCCGGCT  GTCAGCGCAG  GGGCGCCCGG  TTCTTTTTGT  CAAGACCGAC
       ACAAGGCCGA  CAGTCGCGTC  CCCGCGGGCC  AAGAAAAACA  GTTCTGGCTG
-------------------------------------------------------------------

5201   CTGTCCGGTG  CCCTGAATGA  ACTGCAGGAC  GAGGCAGCGC  GGCTATCGTG
       GACAGGCCAC  GGGACTTACT  TGACGTCCTG  CTCCGTCGCG  CCGATAGCAC
-------------------------------------------------------------------

5251   GCTGGCCACG  ACGGGCGTTC  CTTGCGCAGC  TGTGCTCGAC  GTTGTCACTG
       CGACCGGTGC  TGCCCGCAAG  GAACGCGTCG  ACACGAGCTG  CAACAGTGAC
-------------------------------------------------------------------

5301   AAGCGGGAAG  GGACTGGCTG  CTATTGGGCG  AAGTGCCGGG  GCAGGATCTC
       TTCGCCCTTC  CCTGACCGAC  GATAACCCGC  TTCACGGCCC  CGTCCTAGAG
-------------------------------------------------------------------

5351   CTGTCATCTC  ACCTTGCTCC  TGCCGAGAAA  GTATCCATCA  TGGCTGATGC
       GACAGTAGAG  TGGAACGAGG  ACGGCTCTTT  CATAGGTAGT  ACCGACTACG
-------------------------------------------------------------------

5401   AATGCGGCGG  CTGCATACGC  TTGATCCGGC  TACCTGCCCA  TTCGACCACC
       TTACGCCGCC  GACGTATGCG  AACTAGGCCG  ATGGACGGGT  AAGCTGGTGG
-------------------------------------------------------------------

5451   AAGCGAAACA  TCGCATCGAG  CGAGCACGTA  CTCGGATGGA  AGCCGGTCTT
       TTCGCTTTGT  AGCGTAGCTC  GCTCGTGCAT  GAGCCTACCT  TCGGCCAGAA
-------------------------------------------------------------------

5501   GTCGATCAGG  ATGATCTGGA  CGAAGAGCAT  CAGGGGCTCG  CGCCAGCCGA
       CAGCTAGTCC  TACTAGACCT  GCTTCTCGTA  GTCCCCGAGC  GCGGTCGGCT
-------------------------------------------------------------------

5551   ACTGTTCGCC  AGGCTCAAGG  CGCGCATGCC  CGACGGCGAG  GATCTCGTCG
       TGACAAGCGG  TCCGAGTTCC  GCGCGTACGG  GCTGCCGCTC  CTAGAGCAGC
-------------------------------------------------------------------

5601   TGACCCATGG  CGATGCCTGC  TTGCCGAATA  TCATGGTGGA  AAATGGCCGC
       ACTGGGTACC  GCTACGGACG  AACGGCTTAT  AGTACCACCT  TTTACCGGCG
-------------------------------------------------------------------

5651   TTTTCTGGAT  TCATCGACTG  TGGCCGGCTG  GGTGTGGCGG  ACCGCTATCA
       AAAAGACCTA  AGTAGCTGAC  ACCGGCCGAC  CCACACCGCC  TGGCGATAGT
-------------------------------------------------------------------
```

FIG. 11G

```
5701   GGACATAGCG TTGGCTACCC ... GC TGAAGAGCTT GGCGGCGAAT
       CCTGTATCGC AACCGATGGG CACTATAACG ACTTCTCGAA CCGCCGCTTA
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
5751   GGGCTGACCG CTTCCTCGTG CTTTACGGTA TCGCCGCTCC CGATTCGCAG
       CCCGACTGGC GAAGGAGCAC GAAATGCCAT AGCGGCGAGG GCTAAGCGTC
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
5801   CGCATCGCCT TCTATCGCCT TCTTGACGAG TTCTTCTGAG CGGGACTCTG
       GCGTAGCGGA AGATAGCGGA AGAACTGCTC AAGAAGACTC GCCCTGAGAC
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
5851   GGGTTCGCAT CGATAAAATA AAAGATTTTA TTTAGTCTCC AGAAAAAGGG
       CCCAAGCGTA GCTATTTTAT TTTCTAAAAT AAATCAGAGG TCTTTTTCCC
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
5901   GGGAATGAAA GACCCCACCT GTAGGTTTGG CAAGCTAGCT TAAGTAACGC
       CCCTTACTTT CTGGGGTGGA CATCCAAACC GTTCGATCGA ATTCATTGCG
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
5951   CATTTTGCAA GGCATGGAAA AATACATAAC TGAGAATAGA GAAGTTCAGA
       GTAAAACGTT CCGTACCTTT TTATGTATTG ACTCTTATCT CTTCAAGTCT
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
6001   TCAAGGTCAG GAACAGATGG AACAGCTGAA TATGGGCCAA ACAGGATATC
       AGTTCCAGTC CTTGTCTACC TTGTCGACTT ATACCCGGTT TGTCCTATAG
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
6051   TGTGGTAAGC AGTTCCTGCC CCGGCTCAGG GCCAAGAACA GATGGAACAG
       ACACCATTCG TCAAGGACGG GGCCGAGTCC CGGTTCTTGT CTACCTTGTC
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
6101   CTGAATATGG GCCAAACAGG ATATCTGTGG TAAGCAGTTC CTGCCCCGGC
       GACTTATACC CGGTTTGTCC TATAGACACC ATTCGTCAAG GACGGGGCCG
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
6151   TCAGGGCCAA GAACAGATGG TCCCCAGATG CGGTCCAGCC CTCAGCAGTT
       AGTCCCGGTT CTTGTCTACC AGGGGTCTAC GCCAGGTCGG GAGTCGTCAA
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
6201   TCTAGAGAAC CATCAGATGT TTCCAGGGTG CCCCAAGGAC CTGAAATGAC
       AGATCTCTTG GTAGTCTACA AAGGTCCCAC GGGGTTCCTG GACTTTACTG
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
6251   CCTGTGCCTT ATTTGAACTA ACCAATCAGT TCGCTTCTCG CTTCTGTTCG
       GGACACGGAA TAAACTTGAT TGGTTAGTCA AGCGAAGAGC GAAGACAAGC
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
6301   CGCGCTTCTG CTCCCCGAGC TCAATAAAAG AGCCCACAAC CCCTCACTCG
       GCGCGAAGAC GAGGGGCTCG AGTTATTTTC TCGGGTGTTG GGGAGTGAGC
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
6351   GGGCGCCAGT CCTCCGATTG ACTGAGTCGC CCGGGTACCC GTGTATCCAA
       CCCGCGGTCA GGAGGCTAAC TGACTCAGCG GGCCCATGGG CACATAGGTT
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
6401   TAAACCCTCT TGCAGTTGCA TCCGACTTGT GGTCTCGCTG TTCCTTGGGA
       ATTTGGGAGA ACGTCAACGT AGGCTGAACA CCAGAGCGAC AAGGAACCCT
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
6451   GGGTCTCCTC TGAGTGATTG ACTACCCGTC AGCGGGGGTC TTTCATTCAT
       CCCAGAGGAG ACTCACTAAC TGATGGGCAG TCGCCCCCAG AAAGTAAGTA
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
6501   GCAGCATGTA TCAAAATTAA TTTGGTTTTT TTTCTTAAGT ATTTACATTA
       CGTCGTACAT AGTTTTAATT AAACCAAAAA AAAGAATTCA TAAATGTAAT
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
6551   AATGGCCATA GTTGCATTAA TGAATCGGCC AACGCGCGGG GAGAGGCGGT
       TTACCGGTAT CAACGTAATT ACTTAGCCGG TTGCGCGCCC CTCTCCGCCA
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
6601   TTGCGTATTG GCGCTCTTCC GCTTCCTCGC TCACTGACTC GCTGCGCTCG
       AACGCATAAC CGCGAGAAGG CGAAGGAGCG AGTGACTGAG CGACGCGAGC
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
```

FIG. 11 H

```
.6651   GTCGTTCGGC TGCGGCGAGC TGCTATCAGCT CACTCAAAGG CGGTAATACG
        CAGCAAGCCG ACGCCGCTCG CCATAGTCGA GTGAGTTTCC GCCATTATGC

 6701   GTTATCCACA GAATCAGGGG ATAACGCAGG AAAGAACATG TGAGCAAAAG
        CAATAGGTGT CTTAGTCCCC TATTGCGTCC TTTCTTGTAC ACTCGTTTTC

 6751   GCCAGCAAAA GGCCAGGAAC CGTAAAAAGG CCGCGTTGCT GGCGTTTTTC
        CGGTCGTTTT CCGGTCCTTG GCATTTTTCC GGCGCAACGA CCGCAAAAAG

 6801   CATAGGCTCC GCCCCCCTGA CGAGCATCAC AAAAATCGAC GCTCAAGTCA
        GTATCCGAGG CGGGGGGACT GCTCGTAGTG TTTTTAGCTG CGAGTTCAGT

 6851   GAGGTGGCGA AACCCGACAG GACTATAAAG ATACCAGGCG TTTCCCCCTG
        CTCCACCGCT TTGGGCTGTC CTGATATTTC TATGGTCCGC AAAGGGGGAC

 6901   GAAGCTCCCT CGTGCGCTCT CCTGTTCCGA CCCTGCCGCT TACCGGATAC
        CTTCGAGGGA GCACGCGAGA GGACAAGGCT GGGACGGCGA ATGGCCTATG

 6951   CTGTCCGCCT TTCTCCCTTC GGGAAGCGTG GCGCTTTCTC ATAGCTCACG
        GACAGGCGGA AAGAGGGAAG CCCTTCGCAC CGCGAAAGAG TATCGAGTGC

 7001   CTGTAGGTAT CTCAGTTCGG TGTAGGTCGT TCGCTCCAAG CTGGGCTGTG
        GACATCCATA GAGTCAAGCC ACATCCAGCA AGCGAGGTTC GACCCGACAC

 7051   TGCACGAACC CCCCGTTCAG CCCGACCGCT GCGCCTTATC CGGTAACTAT
        ACGTGCTTGG GGGGCAAGTC GGGCTGGCGA CGCGGAATAG GCCATTGATA

 7101   CGTCTTGAGT CCAACCCGGT AAGACACGAC TTATCGCCAC TGGCAGCAGC
        GCAGAACTCA GGTTGGGCCA TTCTGTGCTG AATAGCGGTG ACCGTCGTCG

 7151   CACTGGTAAC AGGATTAGCA GAGCGAGGTA TGTAGGCGGT GCTACAGAGT
        GTGACCATTG TCCTAATCGT CTCGCTCCAT ACATCCGCCA CGATGTCTCA

 7201   TCTTGAAGTG GTGGCCTAAC TACGGCTACA CTAGAAGAAC AGTATTTGGT
        AGAACTTCAC CACCGGATTG ATGCCGATGT GATCTTCTTG TCATAAACCA

 7251   ATCTGCGCTC TGCTGAAGCC AGTTACCTTC GGAAAAAGAG TTGGTAGCTC
        TAGACGCGAG ACGACTTCGG TCAATGGAAG CCTTTTTCTC AACCATCGAG

 7301   TTGATCCGGC AAACAAACCA CCGCTGGTAG CGGTGGTTTT TTTGTTTGCA
        AACTAGGCCG TTTGTTTGGT GGCGACCATC GCCACCAAAA AAACAAACGT

 7351   AGCAGCAGAT TACGCGCAGA AAAAAAGGAT CTCAAGAAGA TCCTTTGATC
        TCGTCGTCTA ATGCGCGTCT TTTTTTCCTA GAGTTCTTCT AGGAAACTAG

 7401   TTTTCTACGG GGTCTGACGC TCAGTGGAAC GAAAACTCAC GTTAAGGGAT
        AAAAGATGCC CCAGACTGCG AGTCACCTTG CTTTTGAGTG CAATTCCCTA

 7451   TTTGGTCATG AGATTATCAA AAAGGATCTT CACCTAGATC CTTTTGCGGC
        AAACCAGTAC TCTAATAGTT TTTCCTAGAA GTGGATCTAG GAAAACGCCG

 7501   CGCAAATCAA TCTAAAGTAT ATATGAGTAA ACTTGGTCTG ACAGTTACCA
        GCGTTTAGTT AGATTTCATA TATACTCATT TGAACCAGAC TGTCAATGGT

 7551   ATGCTTAATC AGTGAGGCAC CTATCTCAGC GATCTGTCTA TTTCGTTCAT
        TACGAATTAG TCACTCCGTG GATAGAGTCG CTAGACAGAT AAAGCAAGTA
```

FIG. 11 I

```
7601  CCATAGTTGC CTGACTCCCG ...TCCGTTAGA TAACTACGAT ACGGGAGGGC
      GGTATCAACG GACTGAGGGG CAGCACATCT ATTGATGCTA TGCCCTCCCG
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
7651  TTACCATCTG GCCCCAGTGC TGCAATGATA CCGCGAGACC CACGCTCACC
      AATGGTAGAC CGGGGTCACG ACGTTACTAT GGCGCTCTGG GTGCGAGTGG
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
7701  GGCTCCAGAT TTATCAGCAA TAAACCAGCC AGCCGGAAGG GCCGAGCGCA
      CCGAGGTCTA AATAGTCGTT ATTTGGTCGG TCGGCCTTCC CGGCTCGCGT
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
7751  GAAGTGGTCC TGCAACTTTA TCCGCCTCCA TCCAGTCTAT TAATTGTTGC
      CTTCACCAGG ACGTTGAAAT AGGCGGAGGT AGGTCAGATA ATTAACAACG
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
7801  CGGGAAGCTA GAGTAAGTAG TTCGCCAGTT AATAGTTTGC GCAACGTTGT
      GCCCTTCGAT CTCATTCATC AAGCGGTCAA TTATCAAACG CGTTGCAACA
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
7851  TGCCATTGCT ACAGGCATCG TGGTGTCACG CTCGTCGTTT GGTATGGCTT
      ACGGTAACGA TGTCCGTAGC ACCACAGTGC GAGCAGCAAA CCATACCGAA
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
7901  CATTCAGCTC CGGTTCCCAA CGATCAAGGC GAGTTACATG ATCCCCCATG
      GTAAGTCGAG GCCAAGGGTT GCTAGTTCCG CTCAATGTAC TAGGGGGTAC
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
7951  TTGTGCAAAA AAGCGGTTAG CTCCTTCGGT CCTCCGATCG TTGTCAGAAG
      AACACGTTTT TTCGCCAATC GAGGAAGCCA GGAGGCTAGC AACAGTCTTC
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
8001  TAAGTTGGCC GCAGTGTTAT CACTCATGGT TATGGCAGCA CTGCATAATT
      ATTCAACCGG CGTCACAATA GTGAGTACCA ATACCGTCGT GACGTATTAA
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
8051  CTCTTACTGT CATGCCATCC GTAAGATGCT TTTCTGTGAC TGGTGAGTAC
      GAGAATGACA GTACGGTAGG CATTCTACGA AAAGACACTG ACCACTCATG
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
8101  TCAACCAAGT CATTCTGAGA ATAGTGTATG CGGCGACCGA GTTGCTCTTG
      AGTTGGTTCA GTAAGACTCT TATCACATAC GCCGCTGGCT CAACGAGAAC
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
8151  CCCGGCGTCA ATACGGGATA ATACCGCGCC ACATAGCAGA ACTTTAAAAG
      GGGCCGCAGT TATGCCCTAT TATGGCGCGG TGTATCGTCT TGAAATTTTC
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
8201  TGCTCATCAT TGGAAAACGT TCTTCGGGGC GAAAACTCTC AAGGATCTTA
      ACGAGTAGTA ACCTTTTGCA AGAAGCCCCG CTTTTGAGAG TTCCTAGAAT
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
8251  CCGCTGTTGA GATCCAGTTC GATGTAACCC ACTCGTGCAC CCAACTGATC
      GGCGACAACT CTAGGTCAAG CTACATTGGG TGAGCACGTG GGTTGACTAG
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
8301  TTCAGCATCT TTTACTTTCA CCAGCGTTTC TGGGTGAGCA AAAACAGGAA
      AAGTCGTAGA AAATGAAAGT GGTCGCAAAG ACCCACTCGT TTTTGTCCTT
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
8351  GGCAAAATGC CGCAAAAAAG GGAATAAGGG CGACACGGAA ATGTTGAATA
      CCGTTTTACG GCGTTTTTTC CCTTATTCCC GCTGTGCCTT TACAACTTAT
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
8401  CTCATACTCT TCCTTTTTCA ATATTATTGA AGCATTTATC AGGGTTATTG
      GAGTATGAGA AGGAAAAAGT TATAATAACT TCGTAAATAG TCCCAATAAC
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
8451  TCTCATGAGC GGATACATAT TTGAATGTAT TTAGAAAAAT AAACAAATAG
      AGAGTACTCG CCTATGTATA AACTTACATA AATCTTTTTA TTTGTTTATC
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
8501  GGGTTCCGCG CACATTTC
      CCCAAGGCGC GTGTAAAG
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
```

FIG. 11J

```
 951   TCCCTTAAGT TTGACCTTAG GTAACTGGAA AGATGTCGAG CGGCTCGCTC
       AGGGAATTCA AACTGGAATC CATTGACCTT TCTACAGCTC GCCGAGCGAG

1001   ACAACCAGTC GGTAGATGTC AAGAAGAGAC GTTGGGTTAC CTTCTGCTCT
       TGTTGGTCAG CCATCTACAG TTCTTCTCTG CAACCCAATG GAAGACGAGA

1051   GCAGAATGGC CAACCTTTAA CGTCGGATGG CCGCGAGACG GCACCTTTAA
       CGTCTTACCG GTTGGAAATT GCAGCCTACC GGCGCTCTGC CGTGGAAATT

1101   CCGAGACCTC ATCACCCAGG TTAAGATCAA GGTCTTTTCA CCTGGCCCGC
       GGCTCTGGAG TAGTGGGTCC AATTCTAGTT CCAGAAAAGT GGACCGGGCG

1151   ATGGACACCC AGACCAGGTC CCCTACATCG TGACCTGGGA AGCCTTGGCT
       TACCTGTGGG TCTGGTCCAG GGGATGTAGC ACTGGACCCT TCGGAACCGA

1201   TTTGACCCCC CTCCCTGGGT CAAGCCCTTT GTACACCCTA AGCCTCCGCC
       AAACTGGGGG GAGGGACCCA GTTCGGGAAA CATGTGGGAT TCGGAGGCGG

1251   TCCTCTTCCT CCATCCGCCC CGTCTCTCCC CCTTGAACCT CCTCGTTCGA
       AGGAGAAGGA GGTAGGCGGG GCAGAGAGGG GGAACTTGGA GGAGCAAGCT

1301   CCCCGCCTCG ATCCTCCCTT TATCCAGCCC TCACTCCTTC TCTAGGCGCC
       GGGGCGGAGC TAGGAGGGAA ATAGGTCGGG AGTGAGGAAG AGATCCGCGG

1351   GGCCGCTCTA GCCCATTAAT ACGACTCACT ATAGGGCGAT TCGAATCAGG
       CCGGCGAGAT CGGGTAATTA TGCTGAGTGA TATCCCGCTA AGCTTAGTCC

1401   CCTTGGCGCG CCGGATCCTT AATTAAGCGC AATTGGGAGG TGGCGGTAGC
       GGAACCGCGC GGCCTAGGAA TTAATTCGCG TTAACCCTCC ACCGCCATCG

1451   CTCGAGATGG GCGTGATTAC GGATTCACTG GCCGTCGTTT TACAACGTCG
       GAGCTCTACC CGCACTAATG CCTAAGTGAC CGGCAGCAAA ATGTTGCAGC

1501   TGACTGGGAA AACCCTGGCG TTACCCAACT TAATCGCCTT GCAGCACATC
       ACTGACCCTT TTGGGACCGC AATGGGTTGA ATTAGCGGAA CGTCGTGTAG

1551   CCCCTTTCGC CAGCTGGCGT AATAGCGAAG AGGCCCGCAC CGATCGCCCT
       GGGGAAAGCG GTCGACCGCA TTATCGCTTC TCCGGGCGTG GCTAGCGGGA

1601   TCCCAACAGT TACGCAGCCT GAATGGCGAA TGGCGCTTTG CCTGGTTTCC
       AGGGTTGTCA ATGCGTCGGA CTTACCGCTT ACCGCGAAAC GGACCAAAGG

1651   GGCACCAGAA GCGGTGCCGG AAAGCTGGCT GGAGTGCGAT CTTCCTGAGG
       CCGTGGTCTT CGCCACGGCC TTTCGACCGA CCTCACGCTA GAAGGACTCC

1701   CCGATACTGT CGTCGTCCCC TCAAACTGGC AGATGCACGG TTACGATGCG
       GGCTATGACA GCAGCAGGGG AGTTTGACCG TCTACGTGCC AATGCTACGC

1751   CCCATCTACA CCAACGTGAC CTATCCCATT ACGGTCAATC CGCCGTTTGT
       GGGTAGATGT GGTTGCACTG GATAGGGTAA TGCCAGTTAG GCGGCAAACA

1801   TCCCACGGAG AATCCGACGG GTTGTTACTC GCTCACATTT AATGTTGATG
       AGGGTGCCTC TTAGGCTGCC CAACAATGAG CGAGTGTAAA TTACAACTAC

1851   AAAGCTGGCT ACAGGAAGGC CAGACGCGAA TTATTTTTGA TGGCGTTAAC
       TTTCGACCGA TGTCCTTCCG GTCTGCGCTT AATAAAAACT ACCGCAATTG
```

FIG. 12C

```
1901  TCGGCGTTTC ATCTGTGGTG CA......... TGGGTCGGTT ACGGCCAGGA
      AGCCGCAAAG TAGACACCAC GTTGCCCGCG ACCCAGCCAA TGCCGGTCCT
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
1951  CAGTCGTTTG CCGTCTGAAT TTGACCTGAG CGCATTTTTA CGCGCCGGAG
      GTCAGCAAAC GGCAGACTTA AACTGGACTC GCGTAAAAAT GCGCGGCCTC
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
2001  AAAACCGCCT CGCGGTGATG GTGCTGCGCT GGAGTGACGG CAGTTATCTG
      TTTTGGCGGA GCGCCACTAC CACGACGCGA CCTCACTGCC GTCAATAGAC
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
2051  GAAGATCAGG ATATGTGGCG GATGAGCGGC ATTTTCCGTG ACGTCTCGTT
      CTTCTAGTCC TATACACCGC CTACTCGCCG TAAAAGGCAC TGCAGAGCAA
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
2101  GCTGCATAAA CCGACTACAC AAATCAGCGA TTTCCATGTT GCCACTCGCT
      CGACGTATTT GGCTGATGTG TTTAGTCGCT AAAGGTACAA CGGTGAGCGA
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
2151  TTAATGATGA TTTCAGCCGC GCTGTACTGG AGGCTGAAGT TCAGATGTGC
      AATTACTACT AAAGTCGGCG CGACATGACC TCCGACTTCA AGTCTACACG
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
2201  GGCGAGTTGC GTGACTACCT ACGGGTAACA GTTTCTTTAT GGCAGGGTGA
      CCGCTCAACG CACTGATGGA TGCCCATTGT CAAAGAAATA CCGTCCCACT
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
2251  AACGCAGGTC GCCAGCGGCA CCGCGCCTTT CGGCGGTGAA ATTATCGATG
      TTGCGTCCAG CGGTCGCCGT GGCGCGGAAA GCCGCCACTT TAATAGCTAC
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
2301  AGCGTGGTGG TTATGCCGAT CGCGTCACAC TACGTCTGAA CGTCGAAAAC
      TCGCACCACC AATACGGCTA GCGCAGTGTG ATGCAGACTT GCAGCTTTTG
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
2351  CCGAAACTGT GGAGCGCCGA AATCCCGAAT CTCTATCGTG CGGTGGTTGA
      GGCTTTGACA CCTCGCGGCT TTAGGGCTTA GAGATAGCAC GCCACCAACT
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
2401  ACTGCACACC GCCGACGGCA CGCTGATTGA AGCAGAAGCC TGCGATGTCG
      TGACGTGTGG CGGCTGCCGT GCGACTAACT TCGTCTTCGG ACGCTACAGC
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
2451  GTTTCCGCGA GGTGCGGATT GAAAATGGTC TGCTGCTGCT GAACGGCAAG
      CAAAGGCGCT CCACGCCTAA CTTTTACCAG ACGACGACGA CTTGCCGTTC
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
2501  CCGTTGCTGA TTCGAGGCGT TAACCGTCAC GAGCATCATC CTCTGCATGG
      GGCAACGACT AAGCTCCGCA ATTGGCAGTG CTCGTAGTAG GAGACGTACC
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
2551  TCAGGTCATG GATGAGCAGA CGATGGTGCA GGATATCCTG CTGATGAAGC
      AGTCCAGTAC CTACTCGTCT GCTACCACGT CCTATAGGAC GACTACTTCG
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
2601  AGAACAACTT TAACGCCGTG CGCTGTTCGC ATTATCCGAA CCATCCGCTG
      TCTTGTTGAA ATTGCGGCAC GCGACAAGCG TAATAGGCTT GGTAGGCGAC
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
2651  TGGTACACGC TGTGCGACCG CTACGGCCTG TATGTGGTGG ATGAAGCCAA
      ACCATGTGCG ACACGCTGGC GATGCCGGAC ATACACCACC TACTTCGGTT
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
2701  TATTGAAACC CACGGCATGG TGCCAATGAA TCGTCTGACC GATGATCCGC
      ATAACTTTGG GTGCCGTACC ACGGTTACTT AGCAGACTGG CTACTAGGCG
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
2751  GCTGGCTACC GGCGATGAGC GAACGCGTAA CGCGAATGGT GCAGCGCGAT
      CGACCGATGG CCGCTACTCG CTTGCGCATT GCGCTTACCA CGTCGCGCTA
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
2801  CGTAATCACC CGAGTGTGAT CATCTGGTCG CTGGGGAATG AATCAGGCCA
      GCATTAGTGG GCTCACACTA GTAGACCAGC GACCCCTTAC TTAGTCCGGT
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
```

FIG. 12D

```
2851  CGGCGCTAAT CACGACGCGC T        GATCAAATCT GTCGATCCTT
      GCCGCGATTA GTGCTGCGCG ACATAGCGAC CTAGTTTAGA CAGCTAGGAA
--------------------------------------------------------------------
2901  CCCGCCCGGT GCAGTATGAA GGCGGCGGAG CCGACACCAC GGCCACCGAT
      GGGCGGGCCA CGTCATACTT CCGCCGCCTC GGCTGTGGTG CCGGTGGCTA
--------------------------------------------------------------------
2951  ATTATTTGCC CGATGTACGC GCGCGTGGAT GAAGACCAGC CCTTCCCGGC
      TAATAAACGG GCTACATGCG CGCGCACCTA CTTCTGGTCG GGAAGGGCCG
--------------------------------------------------------------------
3001  TGTGCCGAAA TGGTCCATCA AAAAATGGCT TTCGCTACCT GGAGAGACGC
      ACACGGCTTT ACCAGGTAGT TTTTTACCGA AAGCGATGGA CCTCTCTGCG
--------------------------------------------------------------------
3051  GCCCGCTGAT CCTTTGCGAA TACGCCCACG CGATGGGTAA CAGTCTTGGC
      CGGGCGACTA GGAAACGCTT ATGCGGGTGC GCTACCCATT GTCAGAACCG
--------------------------------------------------------------------
3101  GGTTTCGCTA AATACTGGCA GGCGTTTCGT CAGTATCCCC GTTTACAGGG
      CCAAAGCGAT TTATGACCGT CCGCAAAGCA GTCATAGGGG CAAATGTCCC
--------------------------------------------------------------------
3151  CGGCTTCGTC TGGGACTGGG TGGATCAGTC GCTGATTAAA TATGATGAAA
      GCCGAAGCAG ACCCTGACCC ACCTAGTCAG CGACTAATTT ATACTACTTT
--------------------------------------------------------------------
3201  ACGGCAACCC GTGGTCGGCT TACGGCGGTG ATTTTGGCGA TACGCCGAAC
      TGCCGTTGGG CACCAGCCGA ATGCCGCCAC TAAAACCGCT ATGCGGCTTG
--------------------------------------------------------------------
3251  GATCGCCAGT TCTGTATGAA CGGTCTGGTC TTTGCCGACC GCACGCCGCA
      CTAGCGGTCA AGACATACTT GCCAGACCAG AAACGGCTGG CGTGCGGCGT
--------------------------------------------------------------------
3301  TCCAGCGCTG ACGGAAGCAA AACACCAGCA GCAGTTTTTC CAGTTCCGTT
      AGGTCGCGAC TGCCTTCGTT TTGTGGTCGT CGTCAAAAAG GTCAAGGCAA
--------------------------------------------------------------------
3351  TATCCGGGCA AACCATCGAA GTGACCAGCG AATACCTGTT CCGTCATAGC
      ATAGGCCCGT TTGGTAGCTT CACTGGTCGC TTATGGACAA GGCAGTATCG
--------------------------------------------------------------------
3401  GATAACGAGC TCCTGCACTG GATGGTGGCG CTGGATGGTA AGCCGCTGGC
      CTATTGCTCG AGGACGTGAC CTACCACCGC GACCTACCAT TCGGCGACCG
--------------------------------------------------------------------
3451  AAGCGGTGAA GTGCCTCTGG ATGTCGCTCC ACAAGGTAAA CAGTTGATTG
      TTCGCCACTT CACGGAGACC TACAGCGAGG TGTTCCATTT GTCAACTAAC
--------------------------------------------------------------------
3501  AACTGCCTGA ACTACCGCAG CCGGAGAGCG CCGGGCAACT CTGGCTCACA
      TTGACGGACT TGATGGCGTC GGCCTCTCGC GGCCCGTTGA GACCGAGTGT
--------------------------------------------------------------------
3551  GTACGCGTAG TGCAACCGAA CGCGACCGCA TGGTCAGAAG CCGGGCACAT
      CATGCGCATC ACGTTGGCTT GCGCTGGCGT ACCAGTCTTC GGCCCGTGTA
--------------------------------------------------------------------
3601  CAGCGCCTGG CAGCAGTGGC GTCTGGCGGA AAACCTCAGT GTGACGCTCC
      GTCGCGGACC GTCGTCACCG CAGACCGCCT TTTGGAGTCA CACTGCGAGG
--------------------------------------------------------------------
3651  CCGCCGCGTC CCACGCCATC CCGCATCTGA CCACCAGCGA AATGGATTTT
      GGCGGCGCAG GGTGCGGTAG GGCGTAGACT GGTGGTCGCT TTACCTAAAA
--------------------------------------------------------------------
3701  TGCATCGAGC TGGGTAATAA GCGTTGGCAA TTTAACCGCC AGTCAGGCTT
      ACGTAGCTCG ACCCATTATT CGCAACCGTT AAATTGGCGG TCAGTCCGAA
--------------------------------------------------------------------
3751  TCTTTCACAG ATGTGGATTG GCGATAAAAA ACAACTGCTG ACGCCGCTGC
      AGAAAGTGTC TACACCTAAC CGCTATTTTT TGTTGACGAC TGCGGCGACG
--------------------------------------------------------------------
```

FIG. 12E

```
3801  GCGATCAGTT CACCCGTGTC GGTGATCGTG AACAGAAACT CATTTCCGAA
      CGCTAGTCAA GTGGGCACAG CTATCTAGAC TTGTCTTTGA GTAAAGGCTT
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
3851  GAAGACCTAG TCGACCATCA TCATCATCAT CACCGGTAAT AATAGGTAGA
      CTTCTGGATC AGCTGGTAGT AGTAGTAGTA GTGGCCATTA TTATCCATCT
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
3901  TAAGTGACTG ATTAGATGCA TTTCGACTAG ATCCCTCGAC CAATTCCGGT
      ATTCACTGAC TAATCTACGT AAAGCTGATC TAGGGAGCTG GTTAAGGCCA
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
3951  TATTTTCCAC CATATTGCCG TCTTTTGGCA ATGTGAGGGC CCGGAAACCT
      ATAAAAGGTG GTATAACGGC AGAAAACCGT TACACTCCCG GGCCTTTGGA
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
4001  GGCCCTGTCT TCTTGACGAG CATTCCTAGG GGTCTTTCCC CTCTCGCCAA
      CCGGGACAGA AGAACTGCTC GTAAGGATCC CCAGAAAGGG GAGAGCGGTT
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
4051  AGGAATGCAA GGTCTGTTGA ATGTCGTGAA GGAAGCAGTT CCTCTGGAAG
      TCCTTACGTT CCAGACAACT TACAGCACTT CCTTCGTCAA GGAGACCTTC
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
4101  CTTCTTGAAG ACAAACAACG TCTGTAGCGA CCCTTTGCAG GCAGCGGAAC
      GAAGAACTTC TGTTTGTTGC AGACATCGCT GGGAAACGTC CGTCGCCTTG
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
4151  CCCCCACCTG GCGACAGGTG CCTCTGCGGC CAAAAGCCAC GTGTATAAGA
      GGGGGTGGAC CGCTGTCCAC GGAGACGCCG GTTTTCGGTG CACATATTCT
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
4201  TACACCTGCA AAGGCGGCAC AACCCCAGTG CCACGTTGTG AGTTGGATAG
      ATGTGGACGT TTCCGCCGTG TTGGGGTCAC GGTGCAACAC TCAACCTATC
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
4251  TTGTGGAAAG AGTCAAATGG CTCTCCTCAA GCGTATTCAA CAAGGGGCTG
      AACACCTTTC TCAGTTTACC GAGAGGAGTT CGCATAAGTT GTTCCCCGAC
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
4301  AAGGATGCCC AGAAGGTACC CCATTGTATG GGATCTGATC TGGGGCCTCG
      TTCCTACGGG TCTTCCATGG GGTAACATAC CCTAGACTAG ACCCCGGAGC
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
4351  GTGCACATGC TTTACATGTG TTTAGTCGAG GTTAAAAAAC GTCTAGGCCC
      CACGTGTACG AAATGTACAC AAATCAGCTC CAATTTTTTG CAGATCCGGG
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
4401  CCCGAACCAC GGGGACGTGG TTTTCCTTTG AAAAACACGA TGATAATACC
      GGGCTTGGTG CCCCTGCACC AAAAGGAAAC TTTTTGTGCT ACTATTATGG
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
4451  ATGAAAAAGC CTGAACTCAC CGCGACGTCT GTCGAGAAGT TTCTGATCGA
      TACTTTTTCG GACTTGAGTG GCGCTGCAGA CAGCTCTTCA AAGACTAGCT
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
4501  AAAGTTCGAC AGCGTCTCCG ACCTGATGCA GCTCTCGGAG GGCGAAGAAT
      TTTCAAGCTG TCGCAGAGGC TGGACTACGT CGAGAGCCTC CCGCTTCTTA
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
4551  CTCGTGCTTT CAGCTTCGAT GTAGGAGGGC GTGGATATGT CCTGCGGGTA
      GAGCACGAAA GTCGAAGCTA CATCCTCCCG CACCTATACA GGACGCCCAT
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
4601  AATAGCTGCG CCGATGGTTT CTACAAAGAT CGTTATGTTT ATCGGCACTT
      TTATCGACGC GGCTACCAAA GATGTTTCTA GCAATACAAA TAGCCGTGAA
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
4651  TGCATCGGCC GCGCTCCCGA TTCCGGAAGT GCTTGACATT GGGGAATTTA
      ACGTAGCCGG CGCGAGGGCT AAGGCCTTCA CGAACTGTAA CCCCTTAAAT
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
4701  GCGAGAGCCT GACCTATTGC ATCTCCCGCC GTGCACAGGG TGTCACGTTG
      CGCTCTCGGA CTGGATAACG TAGAGGGCGG CACGTGTCCC ACAGTGCAAC
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
```

FIG. 12F

```
4751  CAAGACCTGC CTGAAACCGA TAAGCCCGCT GTTCTGCAGC CGGTCGCGGA
      GTTCTGGACG GACTTTGGCT TGACGGGCGA CAAGACGTCG GCCAGCGCCT
```

```
4801  GGCCATGGAT GCGATCGCTG CGGCCGATCT TAGCCAGACG AGCGGGTTCG
      CCGGTACCTA CGCTAGCGAC GCCGGCTAGA ATCGGTCTGC TCGCCCAAGC
```

```
4851  GCCCATTCGG ACCGCAAGGA ATCGGTCAAT ACACTACATG GCGTGATTTC
      CGGGTAAGCC TGGCGTTCCT TAGCCAGTTA TGTGATGTAC CGCACTAAAG
```

```
4901  ATATGCGCGA TTGCTGATCC CCATGTGTAT CACTGGCAAA CTGTGATGGA
      TATACGCGCT AACGACTAGG GGTACACATA GTGACCGTTT GACACTACCT
```

```
4951  CGACACCGTC AGTGCGTCCG TCGCGCAGGC TCTCGATGAG CTGATGCTTT
      GCTGTGGCAG TCACGCAGGC AGCGCGTCCG AGAGCTACTC GACTACGAAA
```

```
5001  GGGCCGAGGA CTGCCCCGAA GTCCGGCACC TCGTGCACGC GGATTTCGGC
      CCCGGCTCCT GACGGGGCTT CAGGCCGTGG AGCACGTGCG CCTAAAGCCG
```

```
5051  TCCAACAATG TCCTGACGGA CAATGGCCGC ATAACAGCGG TCATTGACTG
      AGGTTGTTAC AGGACTGCCT GTTACCGGCG TATTGTCGCC AGTAACTGAC
```

```
5101  GAGCGAGGCG ATGTTCGGGG ATTCCCAATA CGAGGTCGCC AACATCTTCT
      CTCGCTCCGC TACAAGCCCC TAAGGGTTAT GCTCCAGCGG TTGTAGAAGA
```

```
5151  TCTGGAGGCC GTGGTTGGCT TGTATGGAGC AGCAGACGCG CTACTTCGAG
      AGACCTCCGG CACCAACCGA ACATACCTCG TCGTCTGCGC GATGAAGCTC
```

```
5201  CGGAGGCATC CGGAGCTTGC AGGATCGCCG CGGCTCCGGG CGTATATGCT
      GCCTCCGTAG GCCTCGAACG TCCTAGCGGC GCCGAGGCCC GCATATACGA
```

```
5251  CCGCATTGGT CTTGACCAAC TCTATCAGAG CTTGGTTGAC GGCAATTTCG
      GGCGTAACCA GAACTGGTTG AGATAGTCTC GAACCAACTG CCGTTAAAGC
```

```
5301  ATGATGCAGC TTGGGCGCAG GGTCGATGCG ACGCAATCGT CCGATCCGGA
      TACTACGTCG AACCCGCGTC CCAGCTACGC TGCGTTAGCA GGCTAGGCCT
```

```
5351  GCCGGGACTG TCGGGCGTAC ACAAATCGCC CGCAGAAGCG CGGCCGTCTG
      CGGCCCTGAC AGCCCGCATG TGTTTAGCGG GCGTCTTCGC GCCGGCAGAC
```

```
5401  GACCGATGGC TGTGTAGAAG TACTCGCCGA TAGTGGAAAC CGACGCCCCA
      CTGGCTACCG ACACATCTTC ATGAGCGGCT ATCACCTTTG GCTGCGGGGT
```

```
5451  GCACTCGTCC GAGGGCAAAG GAATAGAGTA GATGCCGACC GGGATCTATC
      CGTGAGCAGG CTCCCGTTTC CTTATCTCAT CTACGGCTGG CCCTAGATAG
```

```
5501  GATAAAATAA AAGATTTTAT TTAGTCTCCA GAAAAAGGGG GGAATGAAAG
      CTATTTTATT TTCTAAAATA AATCAGAGGT CTTTTTCCCC CCTTACTTTC
```

```
5551  ACCCCACCTG TAGGTTTGGC AAGCTAGCTT AAGTAACGCC ATTTTGCAAG
      TGGGGTGGAC ATCCAAACCG TTCGATCGAA TTCATTGCGG TAAAACGTTC
```

```
5601  GCATGGAAAA ATACATAACT GAGAATAGAG AAGTTCAGAT CAAGGTCAGG
      CGTACCTTTT TATGTATTGA CTCTTATCTC TTCAAGTCTA GTTCCAGTCC
```

```
5651  AACAGATGGA ACAGCTGAAT ATGGGCCAAA CAGGATATCT GTGGTAAGCA
      TTGTCTACCT TGTCGACTTA TACCCGGTTT GTCCTATAGA CACCATTCGT
```

FIG. 12G

```
5701  GTTCCTGCCC CGGCTCAGGG TGARGACAG ATGGAACAGC TGAATATGGG
      CAAGGACGGG GCCGAGTCCC GGTTCTTGTC TACCTTGTCG ACTTATACCC
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
5751  CCAAACAGGA TATCTGTGGT AAGCAGTTCC TGCCCCGGCT CAGGGCCAAG
      GGTTTGTCCT ATAGACACCA TTCGTCAAGG ACGGGGCCGA GTCCCGGTTC
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
5801  AACAGATGGT CCCCAGATGC GGTCCAGCCC TCAGCAGTTT CTAGAGAACC
      TTGTCTACCA GGGGTCTACG CCAGGTCGGG AGTCGTCAAA GATCTCTTGG
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
5851  ATCAGATGTT TCCAGGGTGC CCCAAGGACC TGAAATGACC CTGTGCCTTA
      TAGTCTACAA AGGTCCCACG GGGTTCCTGG ACTTTACTGG GACACGGAAT
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
5901  TTTGAACTAA CCAATCAGTT CGCTTCTCGC TTCTGTTCGC GCGCTTCTGC
      AAACTTGATT GGTTAGTCAA GCGAAGAGCG AAGACAAGCG CGCGAAGACG
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
5951  TCCCCGAGCT CAATAAAAGA GCCCACAACC CCTCACTCGG GGCGCCAGTC
      AGGGGCTCGA GTTATTTTCT CGGGTGTTGG GGAGTGAGCC CCGCGGTCAG
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
6001  CTCCGATTGA CTGAGTCGCC CGGGTACCCG TGTATCCAAT AAACCCTCTT
      GAGGCTAACT GACTCAGCGG GCCCATGGGC ACATAGGTTA TTTGGGAGAA
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
6051  GCAGTTGCAT CCGACTTGTG GTCTCGCTGT TCCTTGGGAG GGTCTCCTCT
      CGTCAACGTA GGCTGAACAC CAGAGCGACA AGGAACCCTC CCAGAGGAGA
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
6101  GAGTGATTGA CTACCCGTCA GCGGGGGTCT TTCATTCATG CAGCATGTAT
      CTCACTAACT GATGGGCAGT CGCCCCCAGA AAGTAAGTAC GTCGTACATA
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
6151  CAAAATTAAT TTGGTTTTTT TTCTTAAGTA TTTACATTAA ATGGCCATAG
      GTTTTAATTA AACCAAAAAA AAGAATTCAT AAATGTAATT TACCGGTATC
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
6201  TTGCATTAAT GAATCGGCCA ACGCGCGGGG AGAGGCGGTT TGCGTATTGG
      AACGTAATTA CTTAGCCGGT TGCGCGCCCC TCTCCGCCAA ACGCATAACC
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
6251  CGCTCTTCCG CTTCCTCGCT CACTGACTCG CTGCGCTCGG TCGTTCGGCT
      GCGAGAAGGC GAAGGAGCGA GTGACTGAGC GACGCGAGCC AGCAAGCCGA
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
6301  GCGGCGAGCG GTATCAGCTC ACTCAAAGGC GGTAATACGG TTATCCACAG
      CGCCGCTCGC CATAGTCGAG TGAGTTTCCG CCATTATGCC AATAGGTGTC
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
6351  AATCAGGGGA TAACGCAGGA AAGAACATGT GAGCAAAAGG CCAGCAAAAG
      TTAGTCCCCT ATTGCGTCCT TTCTTGTACA CTCGTTTTCC GGTCGTTTTC
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
6401  GCCAGGAACC GTAAAAAGGC CGCGTTGCTG GCGTTTTTCC ATAGGCTCCG
      CGGTCCTTGG CATTTTTCCG GCGCAACGAC CGCAAAAAGG TATCCGAGGC
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
6451  CCCCCCTGAC GAGCATCACA AAAATCGACG CTCAAGTCAG AGGTGGCGAA
      GGGGGGACTG CTCGTAGTGT TTTTAGCTGC GAGTTCAGTC TCCACCGCTT
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
6501  ACCCGACAGG ACTATAAAGA TACCAGGCGT TTCCCCCTGG AAGCTCCCTC
      TGGGCTGTCC TGATATTTCT ATGGTCCGCA AAGGGGGACC TTCGAGGGAG
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
6551  GTGCGCTCTC CTGTTCCGAC CCTGCCGCTT ACCGGATACC TGTCCGCCTT
      CACGCGAGAG GACAAGGCTG GGACGGCGAA TGGCCTATGG ACAGGCGGAA
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
6601  TCTCCCTTCG GGAAGCGTGG CGCTTTCTCA TAGCTCACGC TGTAGGTATC
      AGAGGGAAGC CCTTCGCACC GCGAAAGAGT ATCGAGTGCG ACATCCATAG
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
```

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FIG. 12H

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```
6651   TCAGTTCGGT GTAGGT...CCAAGC TGGGCTGTGT GCACGAACCC
       AGTCAAGCCA CATCCAGCAA GCGAGGTTCG ACCCGACACA CGTGCTTGGG
------------------------------------------------------------------------

6701   CCCGTTCAGC CCGACCGCTG CGCCTTATCC GGTAACTATC GTCTTGAGTC
       GGGCAAGTCG GGCTGGCGAC GCGGAATAGG CCATTGATAG CAGAACTCAG
------------------------------------------------------------------------

6751   CAACCCGGTA AGACACGACT TATCGCCACT GGCAGCAGCC ACTGGTAACA
       GTTGGGCCAT TCTGTGCTGA ATAGCGGTGA CCGTCGTCGG TGACCATTGT
------------------------------------------------------------------------

6801   GGATTAGCAG AGCGAGGTAT GTAGGCGGTG CTACAGAGTT CTTGAAGTGG
       CCTAATCGTC TCGCTCCATA CATCCGCCAC GATGTCTCAA GAACTTCACC
------------------------------------------------------------------------

6851   TGGCCTAACT ACGGCTACAC TAGAAGAACA GTATTTGGTA TCTGCGCTCT
       ACCGGATTGA TGCCGATGTG ATCTTCTTGT CATAAACCAT AGACGCGAGA
------------------------------------------------------------------------

6901   GCTGAAGCCA GTTACCTTCG GAAAAAGAGT TGGTAGCTCT TGATCCGGCA
       CGACTTCGGT CAATGGAAGC CTTTTTCTCA ACCATCGAGA ACTAGGCCGT
------------------------------------------------------------------------

6951   AACAAACCAC CGCTGGTAGC GGTGGTTTTT TTGTTTGCAA GCAGCAGATT
       TTGTTTGGTG GCGACCATCG CCACCAAAAA AACAAACGTT CGTCGTCTAA
------------------------------------------------------------------------

7001   ACGCGCAGAA AAAAAGGATC TCAAGAAGAT CCTTTGATCT TTTCTACGGG
       TGCGCGTCTT TTTTTCCTAG AGTTCTTCTA GGAAACTAGA AAAGATGCCC
------------------------------------------------------------------------

7051   GTCTGACGCT CAGTGGAACG AAAACTCACG TTAAGGGATT TTGGTCATGA
       CAGACTGCGA GTCACCTTGC TTTTGAGTGC AATTCCCTAA AACCAGTACT
------------------------------------------------------------------------

7101   GATTATCAAA AAGGATCTTC ACCTAGATCC TTTTAAATTA AAAATGAAGT
       CTAATAGTTT TTCCTAGAAG TGGATCTAGG AAAATTTAAT TTTTACTTCA
------------------------------------------------------------------------

7151   TTGCGGCCGC AAATCAATCT AAAGTATATA TGAGTAAACT TGGTCTGACA
       AACGCCGGCG TTTAGTTAGA TTTCATATAT ACTCATTTGA ACCAGACTGT
------------------------------------------------------------------------

7201   GTTACCAATG CTTAATCAGT GAGGCACCTA TCTCAGCGAT CTGTCTATTT
       CAATGGTTAC GAATTAGTCA CTCCGTGGAT AGAGTCGCTA GACAGATAAA
------------------------------------------------------------------------

7251   CGTTCATCCA TAGTTGCCTG ACTCCCCGTC GTGTAGATAA CTACGATACG
       GCAAGTAGGT ATCAACGGAC TGAGGGGCAG CACATCTATT GATGCTATGC
------------------------------------------------------------------------

7301   GGAGGGCTTA CCATCTGGCC CCAGTGCTGC AATGATACCG CGAGACCCAC
       CCTCCCGAAT GGTAGACCGG GGTCACGACG TTACTATGGC GCTCTGGGTG
------------------------------------------------------------------------

7351   GCTCACCGGC TCCAGATTTA TCAGCAATAA ACCAGCCAGC CGGAAGGGCC
       CGAGTGGCCG AGGTCTAAAT AGTCGTTATT TGGTCGGTCG GCCTTCCCGG
------------------------------------------------------------------------

7401   GAGCGCAGAA GTGGTCCTGC AACTTTATCC GCCTCCATCC AGTCTATTAA
       CTCGCGTCTT CACCAGGACG TTGAAATAGG CGGAGGTAGG TCAGATAATT
------------------------------------------------------------------------

7451   TTGTTGCCGG GAAGCTAGAG TAAGTAGTTC GCCAGTTAAT AGTTTGCGCA
       AACAACGGCC CTTCGATCTC ATTCATCAAG CGGTCAATTA TCAAACGCGT
------------------------------------------------------------------------

7501   ACGTTGTTGC CATTGCTACA GGCATCGTGG TGTCACGCTC GTCGTTTGGT
       TGCAACAACG GTAACGATGT CCGTAGCACC ACAGTGCGAG CAGCAAACCA
------------------------------------------------------------------------

7551   ATGGCTTCAT TCAGCTCCGG TTCCCAACGA TCAAGGCGAG TTACATGATC
       TACCGAAGTA AGTCGAGGCC AAGGGTTGCT AGTTCCGCTC AATGTACTAG
------------------------------------------------------------------------
```
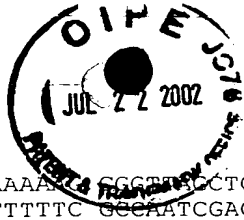
FIG. 12I

```
7601   CCCCATGTTG TGCAAAAA     CTC CTTCGGTCCT CCGATCGTTG
       GGGGTACAAC ACGTTTTTTC     TCGAG GAAGCCAGGA GGCTAGCAAC
--------------------------------------------------------------------------------
7651   TCAGAAGTAA GTTGGCCGCA GTGTTATCAC TCATGGTTAT GGCAGCACTG
       AGTCTTCATT CAACCGGCGT CACAATAGTG AGTACCAATA CCGTCGTGAC
--------------------------------------------------------------------------------
7701   CATAATTCTC TTACTGTCAT GCCATCCGTA AGATGCTTTT CTGTGACTGG
       GTATTAAGAG AATGACAGTA CGGTAGGCAT TCTACGAAAA GACACTGACC
--------------------------------------------------------------------------------
7751   TGAGTACTCA ACCAAGTCAT TCTGAGAATA GTGTATGCGG CGACCGAGTT
       ACTCATGAGT TGGTTCAGTA AGACTCTTAT CACATACGCC GCTGGCTCAA
--------------------------------------------------------------------------------
7801   GCTCTTGCCC GGCGTCAATA CGGGATAATA CCGCGCCACA TAGCAGAACT
       CGAGAACGGG CCGCAGTTAT GCCCTATTAT GGCGCGGTGT ATCGTCTTGA
--------------------------------------------------------------------------------
7851   TTAAAAGTGC TCATCATTGG AAAACGTTCT TCGGGGCGAA AACTCTCAAG
       AATTTTCACG AGTAGTAACC TTTTGCAAGA AGCCCCGCTT TTGAGAGTTC
--------------------------------------------------------------------------------
7901   GATCTTACCG CTGTTGAGAT CCAGTTCGAT GTAACCCACT CGTGCACCCA
       CTAGAATGGC GACAACTCTA GGTCAAGCTA CATTGGGTGA GCACGTGGGT
--------------------------------------------------------------------------------
7951   ACTGATCTTC AGCATCTTTT ACTTTCACCA GCGTTTCTGG GTGAGCAAAA
       TGACTAGAAG TCGTAGAAAA TGAAAGTGGT CGCAAAGACC CACTCGTTTT
--------------------------------------------------------------------------------
8001   ACAGGAAGGC AAAATGCCGC AAAAAAGGGA ATAAGGGCGA CACGGAAATG
       TGTCCTTCCG TTTTACGGCG TTTTTTCCCT TATTCCCGCT GTGCCTTTAC
--------------------------------------------------------------------------------
8051   TTGAATACTC ATACTCTTCC TTTTTCAATA TTATTGAAGC ATTTATCAGG
       AACTTATGAG TATGAGAAGG AAAAAGTTAT AATAACTTCG TAAATAGTCC
--------------------------------------------------------------------------------
8101   GTTATTGTCT CATGAGCGGA TACATATTTG AATGTATTTA GAAAAATAAA
       CAATAACAGA GTACTCGCCT ATGTATAAAC TTACATAAAT CTTTTTATTT
--------------------------------------------------------------------------------
8151   CAAATAGGGG TTCCGCGCAC ATTTC
       GTTTATCCCC AAGGCGCGTG TAAAG
--------------------------------------------------------------------------------
```

FIG. 12 J

```
951   TCCCTTAAGT TTGACCTT.......TAACT.C.AA AGATGTCGAG CGGCTCGCTC
      AGGGAATTCA AACTGGAATC ....GACCTT TCTACAGCTC GCCGAGCGAG
------------------------------------------------------------------

1001  ACAACCAGTC GGTAGATGTC AAGAAGAGAC GTTGGGTTAC CTTCTGCTCT
      TGTTGGTCAG CCATCTACAG TTCTTCTCTG CAACCCAATG GAAGACGAGA
------------------------------------------------------------------

1051  GCAGAATGGC CAACCTTTAA CGTCGGATGG CCGCGAGACG GCACCTTTAA
      CGTCTTACCG GTTGGAAATT GCAGCCTACC GGCGCTCTGC CGTGGAAATT
------------------------------------------------------------------

1101  CCGAGACCTC ATCACCCAGG TTAAGATCAA GGTCTTTTCA CCTGGCCCGC
      GGCTCTGGAG TAGTGGGTCC AATTCTAGTT CCAGAAAAGT GGACCGGGCG
------------------------------------------------------------------

1151  ATGGACACCC AGACCAGGTC CCCTACATCG TGACCTGGGA AGCCTTGGCT
      TACCTGTGGG TCTGGTCCAG GGGATGTAGC ACTGGACCCT TCGGAACCGA
------------------------------------------------------------------

1201  TTTGACCCCC CTCCCTGGGT CAAGCCCTTT GTACACCCTA AGCCTCCGCC
      AAACTGGGGG GAGGGACCCA GTTCGGGAAA CATGTGGGAT TCGGAGGCGG
------------------------------------------------------------------

1251  TCCTCTTCCT CCATCCGCCC CGTCTCTCCC CCTTGAACCT CCTCGTTCGA
      AGGAGAAGGA GGTAGGCGGG GCAGAGAGGG GGAACTTGGA GGAGCAAGCT
------------------------------------------------------------------

1301  CCCCGCCTCG ATCCTCCCTT TATCCAGCCC TCACTCCTTC TCTAGGCGCC
      GGGGCGGAGC TAGGAGGGAA ATAGGTCGGG AGTGAGGAAG AGATCCGCGG
------------------------------------------------------------------

1351  GGCCGCTCTA GCCCATTAAT ACGACTCACT ATAGGGCGAT TCGAACACCA
      CCGGCGAGAT CGGGTAATTA TGCTGAGTGA TATCCCGCTA AGCTTGTGGT
------------------------------------------------------------------

1401  TGCACCATCA TCATCATCAC GTCGACGAAC AGAAACTCAT TTCCGAAGAA
      ACGTGGTAGT AGTAGTAGTG CAGCTGCTTG TCTTTGAGTA AAGGCTTCTT
------------------------------------------------------------------

1451  GACCTACTCG AGATGGGCGT GATTACGGAT TCACTGGCCG TCGTTTTACA
      CTGGATGAGC TCTACCCGCA CTAATGCCTA AGTGACCGGC AGCAAAATGT
------------------------------------------------------------------

1501  ACGTCGTGAC TGGGAAAACC CTGGCGTTAC CCAACTTAAT CGCCTTGCAG
      TGCAGCACTG ACCCTTTTGG GACCGCAATG GGTTGAATTA GCGGAACGTC
------------------------------------------------------------------

1551  CACATCCCCC TTTCGCCAGC TGGCGTAATA GCGAAGAGGC CCGCACCGAT
      GTGTAGGGGG AAAGCGGTCG ACCGCATTAT CGCTTCTCCG GGCGTGGCTA
------------------------------------------------------------------

1601  CGCCCTTCCC AACAGTTACG CAGCCTGAAT GGCGAATGGC GCTTTGCCTG
      GCGGGAAGGG TTGTCAATGC GTCGGACTTA CCGCTTACCG CGAAACGGAC
------------------------------------------------------------------

1651  GTTTCCGGCA CCAGAAGCGG TGCCGGAAAG CTGGCTGGAG TGCGATCTTC
      CAAAGGCCGT GGTCTTCGCC ACGGCCTTTC GACCGACCTC ACGCTAGAAG
------------------------------------------------------------------

1701  CTGAGGCCGA TACTGTCGTC GTCCCCTCAA ACTGGCAGAT GCACGGTTAC
      GACTCCGGCT ATGACAGCAG CAGGGGAGTT TGACCGTCTA CGTGCCAATG
------------------------------------------------------------------

1751  GATGCGCCCA TCTACACCAA CGTGACCTAT CCCATTACGG TCAATCCGCC
      CTACGCGGGT AGATGTGGTT GCACTGGATA GGGTAATGCC AGTTAGGCGG
------------------------------------------------------------------

1801  GTTTGTTCCC ACGGAGAATC CGACGGGTTG TTACTCGCTC ACATTTAATG
      CAAACAAGGG TGCCTCTTAG GCTGCCCAAC AATGAGCGAG TGTAAATTAC
------------------------------------------------------------------

1851  TTGATGAAAG CTGGCTACAG GAAGGCCAGA CGCGAATTAT TTTTGATGGC
      AACTACTTTC GACCGATGTC CTTCCGGTCT GCGCTTAATA AAAACTACCG
------------------------------------------------------------------
```

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FIG. 13C   JUL 25 2002

```
1901   GTTAACTCGG CGTTTCATCT GTGGTGCAAC GGGCGCTGGG TCGGTTACGG
       CAATTGAGCC GCAAAGTAGA CACCACGTTG CCCGCGACCC AGCCAATGCC
-----------------------------------------------------------------
1951   CCAGGACAGT CGTTTGCCGT CTGAATTTGA CCTGAGCGCA TTTTTACGCG
       GGTCCTGTCA GCAAACGGCA GACTTAAACT GGACTCGCGT AAAAATGCGC
-----------------------------------------------------------------
2001   CCGGAGAAAA CCGCCTCGCG GTGATGGTGC TGCGCTGGAG TGACGGCAGT
       GGCCTCTTTT GGCGGAGCGC CACTACCACG ACGCGACCTC ACTGCCGTCA
-----------------------------------------------------------------
2051   TATCTGGAAG ATCAGGATAT GTGGCGGATG AGCGGCATTT TCCGTGACGT
       ATAGACCTTC TAGTCCTATA CACCGCCTAC TCGCCGTAAA AGGCACTGCA
-----------------------------------------------------------------
2101   CTCGTTGCTG CATAAACCGA CTACACAAAT CAGCGATTTC CATGTTGCCA
       GAGCAACGAC GTATTTGGCT GATGTGTTTA GTCGCTAAAG GTACAACGGT
-----------------------------------------------------------------
2151   CTCGCTTTAA TGATGATTTC AGCCGCGCTG TACTGGAGGC TGAAGTTCAG
       GAGCGAAATT ACTACTAAAG TCGGCGCGAC ATGACCTCCG ACTTCAAGTC
-----------------------------------------------------------------
2201   ATGTGCGGCG AGTTGCGTGA CTACCTACGG GTAACAGTTT CTTTATGGCA
       TACACGCCGC TCAACGCACT GATGGATGCC CATTGTCAAA GAAATACCGT
-----------------------------------------------------------------
2251   GGGTGAAACG CAGGTCGCCA GCGGCACCGC GCCTTTCGGC GGTGAAATTA
       CCCACTTTGC GTCCAGCGGT CGCCGTGGCG CGGAAAGCCG CCACTTTAAT
-----------------------------------------------------------------
2301   TCGATGAGCG TGGTGGTTAT GCCGATCGCG TCACACTACG TCTGAACGTC
       AGCTACTCGC ACCACCAATA CGGCTAGCGC AGTGTGATGC AGACTTGCAG
-----------------------------------------------------------------
2351   GAAAACCCGA AACTGTGGAG CGCCGAAATC CCGAATCTCT ATCGTGCGGT
       CTTTTGGGCT TTGACACCTC GCGGCTTTAG GGCTTAGAGA TAGCACGCCA
-----------------------------------------------------------------
2401   GGTTGAACTG CACACCGCCG ACGGCACGCT GATTGAAGCA GAAGCCTGCG
       CCAACTTGAC GTGTGGCGGC TGCCGTGCGA CTAACTTCGT CTTCGGACGC
-----------------------------------------------------------------
2451   ATGTCGGTTT CCGCGAGGTG CGGATTGAAA ATGGTCTGCT GCTGCTGAAC
       TACAGCCAAA GGCGCTCCAC GCCTAACTTT TACCAGACGA CGACGACTTG
-----------------------------------------------------------------
2501   GGCAAGCCGT TGCTGATTCG AGGCGTTAAC CGTCACGAGC ATCATCCTCT
       CCGTTCGGCA ACGACTAAGC TCCGCAATTG GCAGTGCTCG TAGTAGGAGA
-----------------------------------------------------------------
2551   GCATGGTCAG GTCATGGATG AGCAGACGAT GGTGCAGGAT ATCCTGCTGA
       CGTACCAGTC CAGTACCTAC TCGTCTGCTA CCACGTCCTA TAGGACGACT
-----------------------------------------------------------------
2601   TGAAGCAGAA CAACTTTAAC GCCGTGCGCT GTTCGCATTA TCCGAACCAT
       ACTTCGTCTT GTTGAAATTG CGGCACGCGA CAAGCGTAAT AGGCTTGGTA
-----------------------------------------------------------------
2651   CCGCTGTGGT ACACGCTGTG CGACCGCTAC GGCCTGTATG TGGTGGATGA
       GGCGACACCA TGTGCGACAC GCTGGCGATG CCGGACATAC ACCACCTACT
-----------------------------------------------------------------
2701   AGCCAATATT GAAACCCACG GCATGGTGCC AATGAATCGT CTGACCGATG
       TCGGTTATAA CTTTGGGTGC CGTACCACGG TTACTTAGCA GACTGGCTAC
-----------------------------------------------------------------
2751   ATCCGCGCTG GCTACCGGCG ATGAGCGAAC GCGTAACGCG AATGGTGCAG
       TAGGCGCGAC CGATGGCCGC TACTCGCTTG CGCATTGCGC TTACCACGTC
-----------------------------------------------------------------
2801   CGCGATCGTA ATCACCCGAG TGTGATCATC TGGTCGCTGG GGAATGAATC
       GCGCTAGCAT TAGTGGGCTC ACACTAGTAG ACCAGCGACC CCTTACTTAG
-----------------------------------------------------------------
```
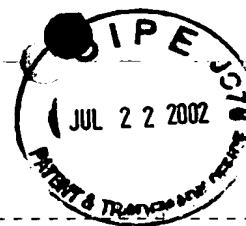
FIG. 13 D

```
2851  AGGCCACGGC GCTAATCACG ACGCGCTGTA TCGCTGGATC AAATCTGTCG
      TCCGGTGCCG CGATTAGTGC TGCGCGACAT AGCGACCTAG TTTAGACAGC

2901  ATCCTTCCCG CCCGGTGCAG TATGAAGGCG GCGGAGCCGA CACCCACGGCC
      TAGGAAGGGC GGGCCACGTC ATACTTCCGC CGCCTCGGCT GTGGTGCCGG

2951  ACCGATATTA TTTGCCCGAT GTACGCGCGC GTGGATGAAG ACCAGCCCTT
      TGGCTATAAT AAACGGGCTA CATGCGCGCG CACCTACTTC TGGTCGGGAA

3001  CCCGGCTGTG CCGAAATGGT CCATCAAAAA ATGGCTTTCG CTACCTGGAG
      GGGCCGACAC GGCTTTACCA GGTAGTTTTT TACCGAAAGC GATGGACCTC

3051  AGACGCGCCC GCTGATCCTT TGCGAATACG CCCACGCGAT GGGTAACAGT
      TCTGCGCGGG CGACTAGGAA ACGCTTATGC GGGTGCGCTA CCCATTGTCA

3101  CTTGGCGGTT TCGCTAAATA CTGGCAGGCG TTTCGTCAGT ATCCCCGTTT
      GAACCGCCAA AGCGATTTAT GACCGTCCGC AAAGCAGTCA TAGGGGCAAA

3151  ACAGGGCGGC TTCGTCTGGG ACTGGGTGGA TCAGTCGCTG ATTAAATATG
      TGTCCCGCCG AAGCAGACCC TGACCCACCT AGTCAGCGAC TAATTTATAC

3201  ATGAAAACGG CAACCCGTGG TCGGCTTACG GCGGTGATTT TGGCGATACG
      TACTTTTGCC GTTGGGCACC AGCCGAATGC CGCCACTAAA ACCGCTATGC

3251  CCGAACGATC GCCAGTTCTG TATGAACGGT CTGGTCTTTG CCGACCGCAC
      GGCTTGCTAG CGGTCAAGAC ATACTTGCCA GACCAGAAAC GGCTGGCGTG

3301  GCCGCATCCA GCGCTGACGG AAGCAAAACA CCAGCAGCAG TTTTTCCAGT
      CGGCGTAGGT CGCGACTGCC TTCGTTTTGT GGTCGTCGTC AAAAAGGTCA

3351  TCCGTTTATC CGGGCAAACC ATCGAAGTGA CCAGCGAATA CCTGTTCCGT
      AGGCAAATAG GCCCGTTTGG TAGCTTCACT GGTCGCTTAT GGACAAGGCA

3401  CATAGCGATA ACGAGCTCCT GCACTGGATG GTGGCGCTGG ATGGTAAGCC
      GTATCGCTAT TGCTCGAGGA CGTGACCTAC CACCGCGACC TACCATTCGG

3451  GCTGGCAAGC GGTGAAGTGC CTCTGGATGT CGCTCCACAA GGTAAACAGT
      CGACCGTTCG CCACTTCACG GAGACCTACA GCGAGGTGTT CCATTTGTCA

3501  TGATTGAACT GCCTGAACTA CCGCAGCCGG AGAGCGCCGG GCAACTCTGG
      ACTAACTTGA CGGACTTGAT GGCGTCGGCC TCTCGCGGCC CGTTGAGACC

3551  CTCACAGTAC GCGTAGTGCA ACCGAACGCG ACCGCATGGT CAGAAGCCGG
      GAGTGTCATG CGCATCACGT TGGCTTGCGC TGGCGTACCA GTCTTCGGCC

3601  GCACATCAGC GCCTGGCAGC AGTGGCGTCT GGCGGAAAAC CTCAGTGTGA
      CGTGTAGTCG CGGACCGTCG TCACCGCAGA CCGCCTTTTG GAGTCACACT

3651  CGCTCCCCGC CGCGTCCCAC GCCATCCCGC ATCTGACCAC CAGCGAAATG
      GCGAGGGGCG GCGCAGGGTG CGGTAGGGCG TAGACTGGTG GTCGCTTTAC

3701  GATTTTTGCA TCGAGCTGGG TAATAAGCGT TGGCAATTTA ACCGCCAGTC
      CTAAAAACGT AGCTCGACCC ATTATTCGCA ACCGTTAAAT TGGCGGTCAG

3751  AGGCTTTCTT TCACAGATGT GGATTGGCGA TAAAAAACAA CTGCTGACGC
      TCCGAAAGAA AGTGTCTACA CCTAACCGCT ATTTTTTGTT GACGACTGCG
```
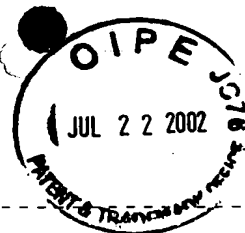
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FIG. 13E   JUL 2 5 2002

```
3801  CGCTGCGCGA TCAGTTCACC CGTGTCGATA GATCTGGAGG TGGTGGCAGC
      GCGACGCGCT AGTCAAGTGG GCACAGCTAT CTAGACCTCC ACCACCGTCG
```

```
3851  AGGCCTTGGC GCGCCGGATC CTTAATTAAC AATTGACCGG TAATAATAGG
      TCCGGAACCG CGCGGCCTAG GAATTAATTG TTAACTGGCC ATTATTATCC
```

```
3901  TAGATAAGTG ACTGATTAGA TGCATTTCGA CTAGATCCCT CGACCAATTC
      ATCTATTCAC TGACTAATCT ACGTAAAGCT GATCTAGGGA GCTGGTTAAG
```

```
3951  CGGTTATTTT CCACCATATT GCCGTCTTTT GGCAATGTGA GGGCCCGGAA
      GCCAATAAAA GGTGGTATAA CGGCAGAAAA CCGTTACACT CCCGGGCCTT
```

```
4001  ACCTGGCCCT GTCTTCTTGA CGAGCATTCC TAGGGGTCTT TCCCCTCTCG
      TGGACCGGGA CAGAAGAACT GCTCGTAAGG ATCCCCAGAA AGGGGAGAGC
```

```
4051  CCAAAGGAAT GCAAGGTCTG TTGAATGTCG TGAAGGAAGC AGTTCCTCTG
      GGTTTCCTTA CGTTCCAGAC AACTTACAGC ACTTCCTTCG TCAAGGAGAC
```

```
4101  GAAGCTTCTT GAAGACAAAC AACGTCTGTA GCGACCCTTT GCAGGCAGCG
      CTTCGAAGAA CTTCTGTTTG TTGCAGACAT CGCTGGGAAA CGTCCGTCGC
```

```
4151  GAACCCCCCA CCTGGCGACA GGTGCCTCTG CGGCCAAAAG CCACGTGTAT
      CTTGGGGGGT GGACCGCTGT CCACGGAGAC GCCGGTTTTC GGTGCACATA
```

```
4201  AAGATACACC TGCAAAGGCG GCACAACCCC AGTGCCACGT TGTGAGTTGG
      TTCTATGTGG ACGTTTCCGC CGTGTTGGGG TCACGGTGCA ACACTCAACC
```

```
4251  ATAGTTGTGG AAAGAGTCAA ATGGCTCTCC TCAAGCGTAT TCAACAAGGG
      TATCAACACC TTTCTCAGTT TACCGAGAGG AGTTCGCATA AGTTGTTCCC
```

```
4301  GCTGAAGGAT GCCCAGAAGG TACCCCATTG TATGGGATCT GATCTGGGGC
      CGACTTCCTA CGGGTCTTCC ATGGGGTAAC ATACCCTAGA CTAGACCCCG
```

```
4351  CTCGGTGCAC ATGCTTTACA TGTGTTTAGT CGAGGTTAAA AAACGTCTAG
      GAGCCACGTG TACGAAATGT ACACAAATCA GCTCCAATTT TTTGCAGATC
```

```
4401  GCCCCCCGAA CCACGGGGAC GTGGTTTTCC TTTGAAAAAC ACGATGATAA
      CGGGGGGCTT GGTGCCCCTG CACCAAAAGG AAACTTTTTG TGCTACTATT
```

```
4451  TACCATGAAA AAGCCTGAAC TCACCGCGAC GTCTGTCGAG AAGTTTCTGA
      ATGGTACTTT TTCGGACTTG AGTGGCGCTG CAGACAGCTC TTCAAAGACT
```

```
4501  TCGAAAAGTT CGACAGCGTC TCCGACCTGA TGCAGCTCTC GGAGGGCGAA
      AGCTTTTCAA GCTGTCGCAG AGGCTGGACT ACGTCGAGAG CCTCCCGCTT
```

```
4551  GAATCTCGTG CTTTCAGCTT CGATGTAGGA GGGCGTGGAT ATGTCCTGCG
      CTTAGAGCAC GAAAGTCGAA GCTACATCCT CCCGCACCTA TACAGGACGC
```

```
4601  GGTAAATAGC TGCGCCGATG GTTTCTACAA AGATCGTTAT GTTTATCGGC
      CCATTTATCG ACGCGGCTAC CAAAGATGTT TCTAGCAATA CAAATAGCCG
```

```
4651  ACTTTGCATC GGCCGCGCTC CCGATTCCGG AAGTGCTTGA CATTGGGGAA
      TGAAACGTAG CCGGCGCGAG GGCTAAGGCC TTCACGAACT GTAACCCCTT
```

```
4701  TTTAGCGAGA GCCTGACCTA TTGCATCTCC CGCCGTGCAC AGGGTGTCAC
      AAATCGCTCT CGGACTGGAT AACGTAGAGG GCGGCACGTG TCCCACAGTG
```
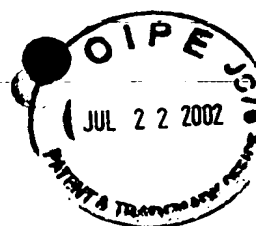
FIG. 13F

```
4751   GTTGCAAGAC CTGCCTGAAA CCGAACTGCC CGCTGTTCTG CAGCCGGTCG
       CAACGTTCTG GACGGACTTT GGCTTGACGG GCGACAAGAC GTCGGCCAGC
-----------------------------------------------------------------
4801   CGGAGGCCAT GGATGCGATC GCTGCGGCCG ATCTTAGCCA GACGAGCGGG
       GCCTCCGGTA CCTACGCTAG CGACGCCGGC TAGAATCGGT CTGCTCGCCC
-----------------------------------------------------------------
4851   TTCGGCCCAT TCGGACCGCA AGGAATCGGT CAATACACTA CATGGCGTGA
       AAGCCGGGTA AGCCTGGCGT TCCTTAGCCA GTTATGTGAT GTACCGCACT
-----------------------------------------------------------------
4901   TTTCATATGC GCGATTGCTG ATCCCCATGT GTATCACTGG CAAACTGTGA
       AAAGTATACG CGCTAACGAC TAGGGGTACA CATAGTGACC GTTTGACACT
-----------------------------------------------------------------
4951   TGGACGACAC CGTCAGTGCG TCCGTCGCGC AGGCTCTCGA TGAGCTGATG
       ACCTGCTGTG GCAGTCACGC AGGCAGCGCG TCCGAGAGCT ACTCGACTAC
-----------------------------------------------------------------
5001   CTTTGGGCCG AGGACTGCCC CGAAGTCCGG CACCTCGTGC ACGCGGATTT
       GAAACCCGGC TCCTGACGGG GCTTCAGGCC GTGGAGCACG TGCGCCTAAA
-----------------------------------------------------------------
5051   CGGCTCCAAC AATGTCCTGA CGGACAATGG CCGCATAACA GCGGTCATTG
       GCCGAGGTTG TTACAGGACT GCCTGTTACC GGCGTATTGT CGCCAGTAAC
-----------------------------------------------------------------
5101   ACTGGAGCGA GGCGATGTTC GGGGATTCCC AATACGAGGT CGCCAACATC
       TGACCTCGCT CCGCTACAAG CCCCTAAGGG TTATGCTCCA GCGGTTGTAG
-----------------------------------------------------------------
5151   TTCTTCTGGA GGCCGTGGTT GGCTTGTATG GAGCAGCAGA CGCGCTACTT
       AAGAAGACCT CCGGCACCAA CCGAACATAC CTCGTCGTCT GCGCGATGAA
-----------------------------------------------------------------
5201   CGAGCGGAGG CATCCGGAGC TTGCAGGATC GCCGCGGCTC CGGGCGTATA
       GCTCGCCTCC GTAGGCCTCG AACGTCCTAG CGGCGCCGAG GCCCGCATAT
-----------------------------------------------------------------
5251   TGCTCCGCAT TGGTCTTGAC CAACTCTATC AGAGCTTGGT TGACGGCAAT
       ACGAGGCGTA ACCAGAACTG GTTGAGATAG TCTCGAACCA ACTGCCGTTA
-----------------------------------------------------------------
5301   TTCGATGATG CAGCTTGGGC GCAGGGTCGA TGCGACGCAA TCGTCCGATC
       AAGCTACTAC GTCGAACCCG CGTCCCAGCT ACGCTGCGTT AGCAGGCTAG
-----------------------------------------------------------------
5351   CGGAGCCGGG ACTGTCGGGC GTACACAAAT CGCCCGCAGA AGCGCGGCCG
       GCCTCGGCCC TGACAGCCCG CATGTGTTTA GCGGGCGTCT TCGCGCCGGC
-----------------------------------------------------------------
5401   TCTGGACCGA TGGCTGTGTA GAAGTACTCG CCGATAGTGG AAACCGACGC
       AGACCTGGCT ACCGACACAT CTTCATGAGC GGCTATCACC TTTGGCTGCG
-----------------------------------------------------------------
5451   CCCAGCACTC GTCCGAGGGC AAAGGAATAG AGTAGATGCC GACCGGGATC
       GGGTCGTGAG CAGGCTCCCG TTTCCTTATC TCATCTACGG CTGGCCCTAG
-----------------------------------------------------------------
5501   TATCGATAAA ATAAAGATT  TTATTTAGTC TCCAGAAAAA GGGGGGAATG
       ATAGCTATTT TATTTTCTAA AATAAATCAG AGGTCTTTTT CCCCCCTTAC
-----------------------------------------------------------------
5551   AAAGACCCCA CCTGTAGGTT TGGCAAGCTA GCTTAAGTAA CGCCATTTTG
       TTTCTGGGGT GGACATCCAA ACCGTTCGAT CGAATTCATT GCGGTAAAAC
-----------------------------------------------------------------
5601   CAAGGCATGG AAAAATACAT AACTGAGAAT AGAGAAGTTC AGATCAAGGT
       GTTCCGTACC TTTTTATGTA TTGACTCTTA TCTCTTCAAG TCTAGTTCCA
-----------------------------------------------------------------
5651   CAGGAACAGA TGGAACAGCT GAATATGGGC CAAACAGGAT ATCTGTGGTA
       GTCCTTGTCT ACCTTGTCGA CTTATACCCG GTTTGTCCTA TAGACACCAT
-----------------------------------------------------------------
```

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FIG. 13G

```
5701  AGCAGTTCCT GCCCCGGCTC AGGGCCAAGA ACAGATGGAA CAGCTGAATA
      TCGTCAAGGA CGGGGCCGAG TCCCGGTTCT TGTCTACCTT GTCGACTTAT

5751  TGGGCCAAAC AGGATATCTG TGGTAAGCAG TTCCTGCCCC GGCTCAGGGC
      ACCCGGTTTG TCCTATAGAC ACCATTCGTC AAGGACGGGG CCGAGTCCCG

5801  CAAGAACAGA TGGTCCCCAG ATGCGGTCCA GCCCTCAGCA GTTTCTAGAG
      GTTCTTGTCT ACCAGGGGTC TACGCCAGGT CGGGAGTCGT CAAAGATCTC

5851  AACCATCAGA TGTTTCCAGG GTGCCCCAAG GACCTGAAAT GACCCTGTGC
      TTGGTAGTCT ACAAAGGTCC CACGGGGTTC CTGGACTTTA CTGGGACACG

5901  CTTATTTGAA CTAACCAATC AGTTCGCTTC TCGCTTCTGT TCGCGCGCTT
      GAATAAACTT GATTGGTTAG TCAAGCGAAG AGCGAAGACA AGCGCGCGAA

5951  CTGCTCCCCG AGCTCAATAA AAGAGCCCAC AACCCCTCAC TCGGGGCGCC
      GACGAGGGGC TCGAGTTATT TTCTCGGGTG TTGGGGAGTG AGCCCCGCGG

6001  AGTCCTCCGA TTGACTGAGT CGCCCGGGTA CCCGTGTATC CAATAAACCC
      TCAGGAGGCT AACTGACTCA GCGGGCCCAT GGGCACATAG GTTATTTGGG

6051  TCTTGCAGTT GCATCCGACT TGTGGTCTCG CTGTTCCTTG GGAGGGTCTC
      AGAACGTCAA CGTAGGCTGA ACACCAGAGC GACAAGGAAC CCTCCCAGAG

6101  CTCTGAGTGA TTGACTACCC GTCAGCGGGG GTCTTTCATT CATGCAGCAT
      GAGACTCACT AACTGATGGG CAGTCGCCCC CAGAAAGTAA GTACGTCGTA

6151  GTATCAAAAT TAATTTGGTT TTTTTTCTTA AGTATTTACA TTAAATGGCC
      CATAGTTTTA ATTAAACCAA AAAAAAGAAT TCATAAATGT AATTTACCGG

6201  ATAGTTGCAT TAATGAATCG GCCAACGCGC GGGGAGAGGC GGTTTGCGTA
      TATCAACGTA ATTACTTAGC CGGTTGCGCG CCCCTCTCCG CCAAACGCAT

6251  TTGGCGCTCT TCCGCTTCCT CGCTCACTGA CTCGCTGCGC TCGGTCGTTC
      AACCGCGAGA AGGCGAAGGA GCGAGTGACT GAGCGACGCG AGCCAGCAAG

6301  GGCTGCGGCG AGCGGTATCA GCTCACTCAA AGGCGGTAAT ACGGTTATCC
      CCGACGCCGC TCGCCATAGT CGAGTGAGTT TCCGCCATTA TGCCAATAGG

6351  ACAGAATCAG GGGATAACGC AGGAAAGAAC ATGTGAGCAA AAGGCCAGCA
      TGTCTTAGTC CCCTATTGCG TCCTTTCTTG TACACTCGTT TTCCGGTCGT

6401  AAAGGCCAGG AACCGTAAAA AGGCCGCGTT GCTGGCGTTT TTCCATAGGC
      TTTCCGGTCC TTGGCATTTT TCCGGCGCAA CGACCGCAAA AAGGTATCCG

6451  TCCGCCCCCC TGACGAGCAT CACAAAAATC GACGCTCAAG TCAGAGGTGG
      AGGCGGGGGG ACTGCTCGTA GTGTTTTTAG CTGCGAGTTC AGTCTCCACC

6501  CGAAACCCGA CAGGACTATA AAGATACCAG GCGTTTCCCC CTGGAAGCTC
      GCTTTGGGCT GTCCTGATAT TTCTATGGTC CGCAAAGGGG GACCTTCGAG

6551  CCTCGTGCGC TCTCCTGTTC CGACCCTGCC GCTTACCGGA TACCTGTCCG
      GGAGCACGCG AGAGGACAAG CTGGGACGG CGAATGGCCT ATGGACAGGC

6601  CCTTTCTCCC TTCGGGAAGC GTGGCGCTTT CTCATAGCTC ACGCTGTAGG
      GGAAAGAGGG AAGCCCTTCG CACCGCGAAA GAGTATCGAG TGCGACATCC
```
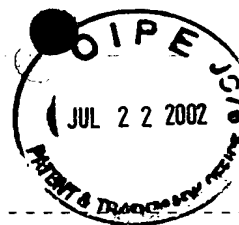
FIG. 13H

```
6651  TATCTCAGTT CGGTGTAGGT CGTTCGCTCC AAGCTGGGCT GTGTGCACGA
      ATAGAGTCAA GCCACATCCA GCAAGCGAGG TTCGACCCGA CACACGTGCT
---------------------------------------------------------------
6701  ACCCCCCGTT CAGCCCGACC GCTGCGCCTT ATCCGGTAAC TATCGTCTTG
      TGGGGGGCAA GTCGGGCTGG CGACGCGGAA TAGGCCATTG ATAGCAGAAC
---------------------------------------------------------------
6751  AGTCCAACCC GGTAAGACAC GACTTATCGC CACTGGCAGC AGCCACTGGT
      TCAGGTTGGG CCATTCTGTG CTGAATAGCG GTGACCGTCG TCGGTGACCA
---------------------------------------------------------------
6801  AACAGGATTA GCAGAGCGAG GTATGTAGGC GGTGCTACAG AGTTCTTGAA
      TTGTCCTAAT CGTCTCGCTC CATACATCCG CCACGATGTC TCAAGAACTT
---------------------------------------------------------------
6851  GTGGTGGCCT AACTACGGCT ACACTAGAAG AACAGTATTT GGTATCTGCG
      CACCACCGGA TTGATGCCGA TGTGATCTTC TTGTCATAAA CCATAGACGC
---------------------------------------------------------------
6901  CTCTGCTGAA GCCAGTTACC TTCGGAAAAA GAGTTGGTAG CTCTTGATCC
      GAGACGACTT CGGTCAATGG AAGCCTTTTT CTCAACCATC GAGAACTAGG
---------------------------------------------------------------
6951  GGCAAACAAA CCACCGCTGG TAGCGGTGGT TTTTTTGTTT GCAAGCAGCA
      CCGTTTGTTT GGTGGCGACC ATCGCCACCA AAAAAACAAA CGTTCGTCGT
---------------------------------------------------------------
7001  GATTACGCGC AGAAAAAAAG GATCTCAAGA AGATCCTTTG ATCTTTTCTA
      CTAATGCGCG TCTTTTTTTC CTAGAGTTCT TCTAGGAAAC TAGAAAAGAT
---------------------------------------------------------------
7051  CGGGGTCTGA CGCTCAGTGG AACGAAAACT CACGTTAAGG GATTTTGGTC
      GCCCCAGACT GCGAGTCACC TTGCTTTTGA GTGCAATTCC CTAAAACCAG
---------------------------------------------------------------
7101  ATGAGATTAT CAAAAAGGAT CTTCACCTAG ATCCTTTTGC GGCCGCAAAT
      TACTCTAATA GTTTTTCCTA GAAGTGGATC TAGGAAAACG CCGGCGTTTA
---------------------------------------------------------------
7151  CAATCTAAAG TATATATGAG TAAACTTGGT CTGACAGTTA CCAATGCTTA
      GTTAGATTTC ATATATACTC ATTTGAACCA GACTGTCAAT GGTTACGAAT
---------------------------------------------------------------
7201  ATCAGTGAGG CACCTATCTC AGCGATCTGT CTATTTCGTT CATCCATAGT
      TAGTCACTCC GTGGATAGAG TCGCTAGACA GATAAAGCAA GTAGGTATCA
---------------------------------------------------------------
7251  TGCCTGACTC CCCGTCGTGT AGATAACTAC GATACGGGAG GGCTTACCAT
      ACGGACTGAG GGGCAGCACA TCTATTGATG CTATGCCCTC CCGAATGGTA
---------------------------------------------------------------
7301  CTGGCCCCAG TGCTGCAATG ATACCGCGAG ACCCACGCTC ACCGGCTCCA
      GACCGGGGTC ACGACGTTAC TATGGCGCTC TGGGTGCGAG TGGCCGAGGT
---------------------------------------------------------------
7351  GATTTATCAG CAATAAACCA GCCAGCCGGA AGGGCCGAGC GCAGAAGTGG
      CTAAATAGTC GTTATTTGGT CGGTCGGCCT TCCCGGCTCG CGTCTTCACC
---------------------------------------------------------------
7401  TCCTGCAACT TTATCCGCCT CCATCCAGTC TATTAATTGT TGCCGGGAAG
      AGGACGTTGA AATAGGCGGA GGTAGGTCAG ATAATTAACA ACGGCCCTTC
---------------------------------------------------------------
7451  CTAGAGTAAG TAGTTCGCCA GTTAATAGTT TGCGCAACGT TGTTGCCATT
      GATCTCATTC ATCAAGCGGT CAATTATCAA ACGCGTTGCA ACAACGGTAA
---------------------------------------------------------------
7501  GCTACAGGCA TCGTGGTGTC ACGCTCGTCG TTTGGTATGG CTTCATTCAG
      CGATGTCCGT AGCACCACAG TGCGAGCAGC AAACCATACC GAAGTAAGTC
---------------------------------------------------------------
7551  CTCCGGTTCC CAACGATCAA GGCGAGTTAC ATGATCCCCC ATGTTGTGCA
      GAGGCCAAGG GTTGCTAGTT CCGCTCAATG TACTAGGGGG TACAACACGT
---------------------------------------------------------------
```
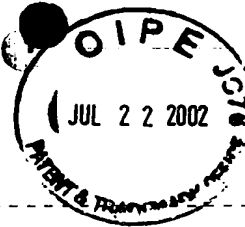
FIG. 13I

```
•7601  AAAAAGCGGT  TAGCTCCTTC  GGTCCTCCGA  TCGTTGTCAG  AAGTAAGTTG
       TTTTTCGCCA  ATCGAGGAAG  CCAGGAGGCT  AGCAACAGTC  TTCATTCAAC
---------------------------------------------------------------------------
 7651  GCCGCAGTGT  TATCACTCAT  GGTTATGGCA  GCACTGCATA  ATTCTCTTAC
       CGGCGTCACA  ATAGTGAGTA  CCAATACCGT  CGTGACGTAT  TAAGAGAATG
---------------------------------------------------------------------------
 7701  TGTCATGCCA  TCCGTAAGAT  GCTTTTCTGT  GACTGGTGAG  TACTCAACCA
       ACAGTACGGT  AGGCATTCTA  CGAAAAGACA  CTGACCACTC  ATGAGTTGGT
---------------------------------------------------------------------------
 7751  AGTCATTCTG  AGAATAGTGT  ATGCGGCGAC  CGAGTTGCTC  TTGCCCGGCG
       TCAGTAAGAC  TCTTATCACA  TACGCCGCTG  GCTCAACGAG  AACGGGCCGC
---------------------------------------------------------------------------
 7801  TCAATACGGG  ATAATACCGC  GCCACATAGC  AGAACTTTAA  AAGTGCTCAT
       AGTTATGCCC  TATTATGGCG  CGGTGTATCG  TCTTGAAATT  TTCACGAGTA
---------------------------------------------------------------------------
 7851  CATTGGAAAA  CGTTCTTCGG  GGCGAAAACT  CTCAAGGATC  TTACCGCTGT
       GTAACCTTTT  GCAAGAAGCC  CCGCTTTTGA  GAGTTCCTAG  AATGGCGACA
---------------------------------------------------------------------------
 7901  TGAGATCCAG  TTCGATGTAA  CCCACTCGTG  CACCCAACTG  ATCTTCAGCA
       ACTCTAGGTC  AAGCTACATT  GGGTGAGCAC  GTGGGTTGAC  TAGAAGTCGT
---------------------------------------------------------------------------
 7951  TCTTTTACTT  TCACCAGCGT  TTCTGGGTGA  GCAAAAACAG  GAAGGCAAAA
       AGAAAATGAA  AGTGGTCGCA  AAGACCCACT  CGTTTTTGTC  CTTCCGTTTT
---------------------------------------------------------------------------
 8001  TGCCGCAAAA  AAGGGAATAA  GGGCGACACG  GAAATGTTGA  ATACTCATAC
       ACGGCGTTTT  TTCCCTTATT  CCCGCTGTGC  CTTTACAACT  TATGAGTATG
---------------------------------------------------------------------------
 8051  TCTTCCTTTT  TCAATATTAT  TGAAGCATTT  ATCAGGGTTA  TTGTCTCATG
       AGAAGGAAAA  AGTTATAATA  ACTTCGTAAA  TAGTCCCAAT  AACAGAGTAC
---------------------------------------------------------------------------
 8101  AGCGGATACA  TATTTGAATG  TATTTAGAAA  AATAAACAAA  TAGGGGTTCC
       TCGCCTATGT  ATAAACTTAC  ATAAATCTTT  TTATTTGTTT  ATCCCCAAGG
---------------------------------------------------------------------------
 8151  GCGCACATTT  C
       CGCGTGTAAA  G
---------------------------------------------------------------------------
```

FIG. 13J